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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 942
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Best Local S
Matches 20
                                                                          Matches
                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            source
                           5473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,NTakeuchi,I., Kohara,Y. and Tanaka,Y.

Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU264231 VS Dictyostelium discoideum cDNA clone VSD554 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 1-1-1 Tennoudai, Tsu
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AU264231
AU264231.1 GI:20523029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Biological Sciences University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
TTTTTTTGTAAAAAGATAATTTTTG 5497
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pump42 (gi14732114|gb]AF122072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                        hideko@biol.tsukuba.ac.jp.
                                                                                                                                                                                                                                                                                    /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                            /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                         /clone="VSD554"
                                                                                                                                                                                                                                                             db_xref="taxon:44689"
                                                                                                                                                                                                                   'sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                              0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%;
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                                                                                              Score 17.6;
Pred. No. 8.
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                                                                        Mismatches
                                                                                              .4e+02;
                                                                                                                    DB 1; Length 26;
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                                                                        5
                                                                        Indels
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KEYWORDS VERSION 밁 S

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FEATURES

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AUTHORS
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VERSION
KEYWORDS
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ORGANISM
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AZ422541
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ORGANISM
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CF302323
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VERSION
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Matches 20
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                                                  Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                         AZ422541 26 bp DNA linear GSS 0: 1M0201G14F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0201G14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _
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               plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Laxge-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF302323 26 bp mRNA linear 7LEAF--07-L19.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--07-L19, mRNA sequence.
CF302323
                                                                                                                                                                                                                                                                                                       AZ422541.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF302323.1 GI:33674084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/db_xref="Nackdong"
/db_xref="Nackdong"
/db_xref="Nackdong"
/clone="7LEAF--07-L19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="B_coli_DH10B"
/clone_lib="Rice leaf plasmid_cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
                                                                                                                                                                                                                                                                                                         GI:10546554
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B. Weiss
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Pred. No. 8.4e+02;
0; Mismatches 4;
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(7LEAF) Oryza
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ACCESSION
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BX550767
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                                                                                                                            TITLE
                                                                                                                                                                             AUTHORS
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                                                                                          Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                         Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX550767 Glossina morsitans morsitans adult infected gut Glossina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0201 row: G column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome University of Utah
                            Genome Biol.
22881942
                                                                                                                                                                                                                                                                                                                                                                                                         morsitans morsitans cDNA clone Tsel14f12_pic, mRNA sequence.
     14519198
                                                                           response genes
                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0201G14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moi_type="genomic DNA"
                                                 4 (10), R63 (2003)
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Pred. No. 8.4e+02;
0; Mismatches 4;
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BX550946
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Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 15A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                    Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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BX550946 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tsel15f11_plc, mRNA sequence.
                                                                                                                                               School of Biological Sciences,
University of Wales,
Bangor LL57 2UM
                                                                                                                                                                                                                                                                                                                                                  14519198
                                                                                                                                                                                                                                                                                                                                                                    response genes
Genome Biol. 4 (10), R63 (2003)
22881942
                                                                                                                                                                                                                                                                                                                                                                                                                                  morsitans morsitans and expression analysis of putative immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Hippoboscoidea, Glossinidae, Glossina.

[ (bases 1 to 27)
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Glossina morsitans morsitans
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Bangor LL57 2UW
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                                                                                                                                                                                                                    Prof. M.J.Lehane
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                                                                                                          clones with suffix q1c are reverse primer reads starting of the cDNA all p1c reads are from
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                                                                                      end.
/organism="Glossina morsitans
/mol_type="mRNA"
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/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans mo:
                                                                    Location/Qualifiers
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|mal_type="mRNA"
|sub_species="morsitans"
|db_xref="taxon:37546"
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Pred. No. 9e+02;
0; Mismatches
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                          morsitans"
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BX551145
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MEDLINE
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Best Local Similarity
Matches 20; Conserv
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University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are r
end of the CDNA all plc reads ar
the 3' end.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Glossina morsitans morsitans
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.
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EST.
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Genome Biol. 4
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TAGATAGTTTTTTTTTTTTTTTT
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                                                                                                                                        /note="country: Zimbabwe; T.brucei"
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T.brucei"
                                                                                                                                                                                                                                                            /organism="Glossina morsitans
/mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                          /clone="Tsel16h03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans moj
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/clone="Tse115f11_pic"
/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
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83.3%;
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                                                                                    Score 17.6; DB : Pred. No. 9e+02;
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Pred. No. 96
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                                                                                                    DB 1;
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                                                                                                  Length 27;
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BX551505
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Best Local Similarity
Matches 20; Conserv
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                                                  AUTHORS
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Glossina morsitans morsitans
Glossina morsitans
Glossina morsitans
Glossina morsitans
Glossina morsitans
Glossina morsitans
Glossina morsitans
Glossina
Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UM
All clones with suffix q1c are reverse primer reads st
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M. Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall, Adult midgut expressed sequence tags from the tsetse fly Gl
                                                                                                                                                                                                                                                                                  BX551505 Glossina morsitans morsitans adult infected gut Glossina
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1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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Pathogen Sequencing Unit
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Genome Biol. 4 (10), R63 (2003)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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/mol_type="mRNA"
/sub_species="morsitans"
/db_xref='taxxon:37546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.brucei"
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/timsue_type="adult infected gut"
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/clone_Tib="Glossina morsitans morsitans adult infected
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                                  School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix alc are
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22881942
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                                                                                                                              Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                           Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Gic morsitans morsitans and expression analysis of putative immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX551552 27 bp mRNA linear EST 10-OCT-20 BX551552 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tsell9c07_plc, mRNA sequence.
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 27)
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BX551552.1 GI:33375771
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22881942
                                                                                                                    Prof. M.J.Lehane
                                                                                                                                                                                                                 Contact: Hall N
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of the cDNA all plc reads are from
3' end.
clones with suffix qlc are reverse primer reads starting of the cDNA all plc reads are from 3^\prime end.
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larity 83.3%;
Conservative
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T.brucei"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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'mol_type="mRNA"
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Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
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The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 18A, UK
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Genome Biol. 4 (10), R63
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All clones w
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T.brucei"
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/clone="Tse119c07_plc"
/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans mo
                                                                                                                                                                                                             /clone="Tsel1c02_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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/mol_type="mRNA"
/sub_species="morsitans"
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/mol_type="mRNA"
/sub_species="morsitans"
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   0;
   Score 17.6; DB 1;
Pred. No. 9e+02;
0; Mismatches 4;
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BX551875
BX551875.1 GI:33376196
EST.
                                                                                                       BX551875 27 bp mRNA linear ESI LU-V
BX551875 Glossina morsitans morsitans adult infected gut Glo
morsitans morsitans cDNA clone Tsel20c06_plc, mRNA sequence.
                                Glossina morsitans morsitans Glossina morsitans
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Bangor LL57 2UW
All clones with suff
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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BX551731 Glossina morsitans morsitans adult infected
morsitans morsitans cDNA clone Tselld03_plc, mRNA sec
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Genome Biol. 4 (10), R63
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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School of Biological Sciences,
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Glossina morsitans morsitans
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|mol_type="mRNA"
|sub_species="morsitans"
|/db_xref="taxon:37546"
|/clone="Tsel1d03_p1c"
|/tissue_type="adult infected gut"
|/clone_Tib="Glossina morsitans morsitans
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nilarity 83.3%;
Conservative
of Biological Sciences,
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Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
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Glossina morsitans morsitans
Glossina morsitans morsitans
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BX551974 Glossina morsitans morsitans adult infected
morsitans morsitans cDNA clone Tse120h02_plc, mRNA se
BX551974
                                                                                                                                                                            response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
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Neopteara, Endopterygota, Diptera, Brachycera,
Hippoboscoidea, Glossinidae, Glossina.
1 (bases 1 to 27)
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1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune
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School of Biological Sciences,
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/tlssue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans
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/mol type="mRNA"
/sub_specise="morsitans"
/db_xref="taxon:37546"
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Bangor LL57 2UW
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University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are
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Genome Biol. 4 (10), R63
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1 (Note: A to 27)
1 (Sares, M.B., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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The Sanger Institute The Wellcome Trust Genome Campus
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Hippoboscoidea; Glossinidae; Glossina.
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Similarity 83.3%;
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/note="country: T.brucei"
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/clone="Tse120h02_plc"
/tlssue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected/clone_Tib="Glossina morsitans morsitans adult infected/clone_Tib="Glossina morsitans morsitans adult infected/clone_Tib="Glossina morsitans morsitans adult infected/clone_Tib="Glossina morsitans morsitans adult infected/clone_Tib="Glossina"
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|sub_species="morsitans"
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                                                                               /clone="Tse121a07_p1c"
/tissue_type="adult infected gut"
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/mol_type="mRNA"
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                                                        lone_lib="Glossina morsitans
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                    EST from adult
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Best Local Similarity
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Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 27)
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morsitans morsitans
BX553159
BX553159.1 GI:33377
                                            8X553159 27 bp mRNA linear I BX553159 Glossina morsitans morsitans adult infected
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
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The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Genome Biol. 4 (10), R63 (2003)
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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/mol_type="mRNA"
/sub_species="morsitans"
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Pred. No. 9e+02;
0; Mismatches
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Pred. No. 96
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Muscomorpha;
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.
1 (bases 1 to 27)
Tohana W Marchen M
                                                                          response genes
Genome Biol. 4 (10),
                                                                                                           Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
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EST.
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University of Wales,
Bangor LL57 2UW
All clones with suffix alc are
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Glossina morsitans morsitans
Glossina morsitans
                      Contact: Hall N
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(bases 1 to 27)
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Conservative
Sequencing Unit
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/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans mo
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/mol_type="mRNA"
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RESULT 959
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                                                                                                                                                                       Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UM
All clones with suffix q1c are reverse primer reads st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehane, M.J., Akaoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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Genome Biol. 4 (10), R63 (2003)
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/organism="Glossina morsitans
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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T.brucei"
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[sub species="morsitans"

/db ref="taxon:37546"

/clone="Tsel28h11 plc"

/tissue type="adult infected gut"

/clone_Tib="Glossina morsitans morsitans adult infected
                                                                                                           ocation/Qualifiers
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9e+02;
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BX553666
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Matches 20
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Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
The Cambridge, CB10 1SA, UK
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                                                                          4 TAGATAGTTTTTTTTTTTTTTT 27
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University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are
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1 (bases 1 to 27)
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/clone_lib="Glossina morsitans morsitans adult infected
gut"
                                                                                                                                                                                                                                                                        /clone="Tse12h08_p1c"
/tlssue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
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T.brucei"
                                                                                                                                                                                                                        /note="country: Zimbabwe;
I.brucei"
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/sub_species="morsitans"
/db_xref="taxon:37546"
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                                                                                                                                                                  Score 17.6; DB Pred. No. 9e+02;
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Pred. No. 9e+02;
                                                                                                                                                 Mismatches
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Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                           Glossina morsitans morsitans
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 27)
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                               Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX554327 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tsel4g09_plc, mRNA sequence.
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1 (bases 1 to 27)
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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/mol_type="mRNA"
/sub_species="morsitans"
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                                                            Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust
Hinxton, Cambridge, CB10 1SA, UK
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Genome Biol. 4 (10), R63 (2003)
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1 (bases 1 to 27)
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Neoptera; Endopterygota; Diptera; Brachycera;
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of the cDNA all plc reads ;
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T.brucei"
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/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans mo
Location/Qualifiers
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/mol_type="mRNA"
/sub_species="morsitans"
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Glossina morsitans morsitans
Glossina morsitans
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Glossina morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

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1 (bases 3 to 27)
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1 (bases 4 to 27)
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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BX555101 Glossina morsitans morsitans adult infected gut Gl
morsitans morsitans cDNA clone Tse19dll_plc, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                      University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                               Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hall N
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/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans mo
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/sub_species="morsitans"
/note="country: Zimbabwe;
r.brucei"
                                                      /tissue type="adult infected gut"
/clone_Tib="Glossina morsitans mo
                                                                             /sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse19d11_p1c"
/tissue_type="adult infected
                                                                                                                                                              /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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University of Wales,

Bangor LL57 2UM

All clones with syft
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BX555155 Glossina morsitans morsitans adult infected gut morsitans morsitans cDNA clone Tse19g11_plc, mRNA sequence
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Genome Biol. 4 (10),
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscc Hippoboscoidea; Glossinidae; Glossina.
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
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Contact: Hall N
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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/tissue type="adult infected gut"
/tione_Tib="Glossina morsitans mo
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/sub_species="mo
                                                                                                                                                                                                                                                                                                                                                                                                                                   note="country: Zimbabwe; EST from adult gut
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/db_xref="taxon:37546"
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                                                            Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
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The Sanger Institute The Wellcome
Hinxton, Cambridge, CB10 1SA, UX
Hinxton, Cambridge, Dlease contact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX555500 27 bp mRNA linear EST 10-OCT-20
BX555500 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21a01_plc, mRNA sequence.
                 Prof. M.J.Lehane
School of Biological Sciences
University of Wales,
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tsetse fly Glossina

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Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Gloss morsitans morsitans and expression analysis of putative immune
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
                                                                                                                                               /clone="Tse20b09_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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/mol_type="mRNA"
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                        Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are
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(bases 1 to 27)

(bases 1 to 27)

Lehane, M. J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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                                       T.brucei"
                                                                                     /clone="Tse21d12_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
                                                                                                                                                           /organism="Glossina morsitans
/mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="country: Zimbabwe;
T.brucei"
                                                                                                                                                                                                                                   ocation/Qualifiers
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clone_lib="Glossina morsitans mo
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/db_kref="taxon:37546"
/clone="Tse21a01_p1c"
/tissue_type="adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>a</u>01
                                                    note="country:
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                                                                                                                                            xref="taxon:37546"
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   0.2%;
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   Score 17.6;
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Length 27;
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Best Local Similarity
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Glossina morsitans morsitans
Glossina morsitans morsitans
Elkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 27)
Lehane, M.J. Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the testse fly Glossina
BX555829.1 GI:33379800
EST.
Glossina morsitans morsitans
                                                                                    BX555829 Glossina morsitans morsitans adult infected gut Glossina
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University of Wales,
Bangor LL57 2UW
All clones with suffix old are
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BX555594 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21f02_p1c, mRNA sequence.
                                                        BX555829
                                                                     morsitans morsitans cDNA clone Tse23b06_plc,
                                                                                                          BX555829
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Pathogen Sequencing Unit
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Genome Biol. 4 (10),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Glossina morsitans
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Tse21f02_p1c"
/tissue_type="adult infected gut"
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/db_xref="taxon:37546"
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University of Wales,
Bangor LL57 20W
All clones with suffix and answering
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Pathogen Sequencing Unit
The Sanger Institute The Well.
Hinxton, Cambridge, CB10 1SA,
                                                                                                                                                    Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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Glossina morsitans morsitans
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Genome Biol. 4 (10), R63
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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1 (bases 1 to 27)
                                                           Contact: Hall N
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Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S.
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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/mol_type="mRNA"
/sub_species="morsitans"
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Pred. No. 9
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                   Genome Campus
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S. and Hall,
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MEDLINE
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                                                                                                                                                                                                                                                                                     Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                       response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S.
Adult midgut expressed sequence tags from the tset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glossina morsitans morsitans
Glossina morsitans morsitans
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University of Wales,
Bangor LL57 2UW
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University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                        14519198
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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BX555901 Glossina morsitans morsitans adult infected gut
morsitans morsitans cDNA clone Tse23f02_plc, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Request for clones, please contact: Mike Lehane
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of the cDNA all p1c reads are from
3' end.
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T.brucei"
/clone="Tse23f02_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                      /mol_type="mRNA"
/sub_species="morsitans"
                                                                                                          organism="Glossina morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="Tse23d05_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
                                                       db_xref="taxon:37546"
                                                                                                                                              location/Qualifiers
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/db_xref="taxon:37546"
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Pred. No. 9
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and Hall,N
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Best Local
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   BX556112
BX556112
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX555930.1 GI:33379899
EST.
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BX555930
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Genome Biol. 4 (10),
22881942
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                                                                                                                                                                                              Similarity
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ilarity 83.3%;
Conservative
                                                                                                                                                                            Conservative
 27 bp mRI
Glossina morsitans morsitans
                                                                                                                                                                                                                                                /note="country: Zimbabwe;
T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="country: T.brucei"
                                                                                                                                                                                                                                                                                                  /clone="Tse23g07 plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans mo
                                                                                                                                                                                                                                                                                                                                                                       organism="Glossina morsitans/mol_type="mRNA"
|sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:37546"
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                                                                                                                                                                              0,
                                                                                                                                                                                             Score 17.6;
Pred. No. 9e
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 linear E
t infected
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                  EST 10-OCT-2003
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AUTHORS
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BX556156
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Best Local 8
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                                        Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Lehane, M.J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                    Glossina morsitans morsitans (Glossina morsitans) Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                             BX556156

27 bp mRNA linear F
BX556156 Glossina morsitans morsitans adult infected
morsitans morsitans cDNA clone Tse25c09_plc, mRNA sec
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Glossina morsitans morsitans
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta,
Neoptera, Endopterygota, Diptera, Brachycera, Muscc
Hippoboscoidea, Glossinidae, Glossina.
                                                                                                                                                                                                             EST.
Glossina morsitans morsitans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   School of Biological Sciences,
University of Wales,
Bangor LL57 20W
All clones with suffix qlc are
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
              Genome
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BX556112
BX556112.1 GI:33380051
                                    response
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Genome Biol. 4 (10), R63 (2003)
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                Biol. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="T8e25a07 p1c"
/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
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/mol_type="mRNA"
/sub_species="morsitans"
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r.brucei"
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                  (10), R63 (2003)
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Pred. No. 9e+0
0; Mismatches
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BX556515
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The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                              Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Meoptera; Endopterygota; Diptera; Brachycera; Musco Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 27)
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                     University of Wales,
Bangor LL57 2UW
                                                                                                                                                      School of Biological Sciences,
                                                                                                                                                                                                                                                        Contact: Hall N
                                                                                                                                                                                                                                                                       14519198
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3' end.
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of the cDNA all plc rea
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ilarity 83.3%;
Conservative
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/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans mo
/organism="Glossina morsitans
/mol_type="mRNA"
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/mol_type="mRNA"
/sub_specise="morsitans"
/db_xref="taxon:37546"
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Muscomorpha;
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AUTHORS
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BX557271
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Query Match
Best Local Similarity
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Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                 Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
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Genome Biol. 4 (10), R63 (2003)
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1 (bases 1 to 27)
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BX557271 Glossina morsitans morsitans adult infected gut Glossina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         morsitans morsitans cDNA clone Tse31c08_p1c,
                                                                                                                                                                                                                                                                                                                                                                                             Bangor LL57
                                                      Similarity
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo:
gut"
                                                                                                               /note="country: Zimbabwe;
T.brucei"
                                                                                                                                                                     /clone="Tse31c08_p1c"
/tissue_type="adult infected
/clone_lib="Glossina morsitar
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/db_xref="taxon:37546"
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/mol_type="mRNA"
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                                   Score 17.6; I
Pred. No. 9e+0
0; Mismatches
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morsitans moi
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AUTHORS
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BX557794
BX557794.1 GI:33428969
EST.
                                          Eukaryota, Metazoa, Arthropoda, Hexapo
Neoptera, Endopterygota, Diptera, Brac
Hippoboscodea, Glossinidae, Glossina.
1 (bases 1 to 27)
                                                                                                                                                                                                           BX557794 27 bp mRNA linear EST 10-OCT-20 EX557794 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse34g04_p1c, mRNA sequence.
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                                                                                                                        Glossina morsitans morsitans
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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Glossina moreitans moreitans
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
                                                                                                                                        Glossina morsitans morsitans
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Similarity 83.3%;
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/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glossina morsitans
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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T.brucei"
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Pred. No. 9e+02;
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                                                                              Hexapoda; Insecta; Pterygota; 
a; Brachycera; Muscomorpha;
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Genome Biol. 4
22881942
                                Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Chane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Hippoboscoidea; Glossinidae; Glossina.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M. J. Lehane
School of Biological Sciences,
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Bangor LL57 2UW
All clones with suff
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/tlssue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans
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'mol type="maka"
'sub specise="morsitans"
'db xref="taxon:37546"
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University of Wales,
Bangor LL57 2UW
All clones with swiffing.
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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/db_xref="taxon:37546"
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/tissue_type="adult infected
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/sub_species="morsitans"
/db_xref="taxon:37546"
                                                                                 /note="country:
                                                                                                                 clone_Tib="Glossina morsitans morsitans adult infected"
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Pred. No. 9e+02;
); Mismatches
                                                                                  Zimbabwe;
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                                                                                 BX560901 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse52f10_plc, mRNA sequence.

BX560901
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 27)
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Genome Biol. 4 (10), R63 (2003)
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               Glossina morsitans morsitans Glossina morsitans
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University of Wales,
Bangor LL57 2UW
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                  BX560901.1
EST.
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxv..../clone="fae4f(0) pic"
/clone="fae4f(0) pic"
/tissue type="adult infected
/clone_Tib="Glossina morsitar
                                                                                                                                                                                                                                                                                                                                                     /note="country: Zimbabwe; T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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Pred. No. 96
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 ISA, UK
Request for Clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                    Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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BX562177.1 GI:33372299
EST
Glossina morsitans morsitans
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Genome Biol. 4 (10), R63
                                                                                                                                                                                           Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
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Genome Biol. 4 (10), R63 (2003)
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                                                                                            Contact: Hall N
                                                                                                                    14519198
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Hippoboscoidea; Glossinidae; Glossina.
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of the cDNA all plc reads are from .
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/mol_type="mRNA"
/sub_species="morsitans"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
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                                                                                                                                                                                                                Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are
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Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygol
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 27)
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The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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22881942
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University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse
All clones with suffix qlc are from
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hall N
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/clone="Tse6f02 plc"
/tlssue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
                                                                                               /organism="Glossina morsitans morsitans"
/moltype="mRNA"
/_____
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/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
                                                           /sub_species="morsitans"
/db_xref="taxon:37546"
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/tissue_type="adult infected gut"
                                                                                                                                                            ocation/Qualifiers
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note="country: Zimbabwe;

EST

from

adult

gut infected with

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RESULT 986
CF328811
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SOURCE
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AZ953355
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VERSION
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Best Local Similarity
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Best Local
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                                                                                                                   27 bp DNA linear GSS 27-APR-20
2M0218M01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0218M01 R, genomic survey sequence
A2953355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University Yongin, Kyeongdi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF328811 27 bp mRNA linear EST NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-009, mRNA sequence.
Mammalia; Eutheria;
1 (bases 1 to 27)
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                               Mus musculus
                                                                                                                 AZ953355
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                                                                Mus musculus (house mouse)
                                                                                                AZ953355.1 GI:13824582
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="NACL--03-009"
                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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Pred. No. 9e+02;
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Pred. No. 9e+02;
0; Mismatches 4;
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CL) Oryza
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                                                                Trypanosoma brucei
Trypanosoma brucei
Hall, N., Bowman, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                            Trypanosoma.
             (bases 1 to 27)
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T. brucei sheared genomic D
genomic survey sequence.
AL472045
AL472045.1 GI:11837399
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 27.
Location/Qualifiers
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Plate: 0218 row: M column: 01
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
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                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTCTTTTCTTTTCTTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTTTTTTTTTTTTTTTTGTC 4486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel elettrophoresis. Vector DNA was prepared from a derivative of phasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NNA and prepared into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Lennard, N.J., Doggett, J., Atkin, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.6;
Pred. No. 9e
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A clone 165h05,
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VERSION
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AW248747
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Best Local Similarity
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JOURNAL
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                      Other EST9: 2821119 5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center: Vector
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: Trace file contained 19 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a xhol site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5473
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AW248747
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2821119.3prime NIH_MGC_7
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making smaller)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hicambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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/mol_type="genomic DNA"
/strain="TREU927"
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/clone="165h05"
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sapiens cDNA clone IMAGE:2821119 3',
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RESULT 990
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Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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14ROOT--02-I08.bl Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-I08, mRNA sequence.
CF291899
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
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/lab host="DH10B (phage-resistant)"
/clome lib="NH1MGC"]"
/clome lib="NH MGC"]"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                      /dev_stage="14 days after germination"
(lab_host="E.coli DH10B"
(clone_lib="Rice root plasmid cDNA library (14ROOT)"
(clone_lib="Rice root plasmid cDNA library (14ROOT)"
(note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                            organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                        /db_xref="taxon:4530"
/clone="14ROOT--02-I08"
/tissue_type="root"
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/clone="IMAGE:2821119"
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|mol_type="mRNA"
                     0.2%;
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                     Score 17.4; DB 1;
Pred. No. 4.6e+02;
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 bp mRNA linear EST 14-AUG-:
14ROOT--02-N17.bl Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-N17, mRNA sequence.
CF292144
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                 1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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CF292072.1 GI:33661105
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                          Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                              Oryza Bativa
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/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT-02-M03"

/tissue_type="root"

/dev_stage="14 days after germination"

/dev_stage="14 days after germination"

/dev_stage="16 days after germination"

/dev_stage="16
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Location/Qualifiers
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Pred. No. 4.6e+02;
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RESULT 993
CF310688/c
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AUTHORS
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Best Local Similarity
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute,
of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
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EST.
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Location/Qualifiers
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                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF--05-H18"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for pCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice root plasmid cDNA library (14ROOT)"
/clone_1lb="Rice root plasmid cDNA library (14ROOT)"
/note="Toetor: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
/mith_oligoribonucleotides and then used as templates for
                                                                                                       /clone lib="ABF3-overexpressing transgenic rice plasmid
                                                                                                                                                  /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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'clone="14ROOT--02-N17"
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Pred. No. 4.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GreenGene Biotech Inc.; Division , MyongJi University
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Query Match

Score 17.4;

DB 1;

Length 19;

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Best Local 9
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CF329136.1
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                                                                                                                                                                                                                                         AZ363907 19 bp DNA linear GSS 0: 1010109113R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0109113 R, genomic survey sequence.
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Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                                                                                                                                                                                                     AZ363907.1 GI:10477607
                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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19 bp mRNA linear EST 18-AUG-2003
NACL--04-F15.bl Rice callus plasmid cDNA library (NACL) Oryza
Sativa cDNA clone NACL--04-F15, mRNA sequence.
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                                                                       (bases 1 to 19)
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                                                                                                                                                             musculus (house mouse)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4530"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/mol_type="mRNA"
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Pred. No. 4.6e+02;
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0; Mismatches 1
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AUTHORS
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                                                                                                                                                                                                                                                           AZ450180

19 bp DNA linear GSS 04-OCT-2000 1M0248K13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0248K13 R, genomic survey sequence.
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                                                                                                                                                                                                                         AZ450180
AZ450180.1 GI:10604710
                                                                                                                                                             Mus musculus
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University of Utah Genome
University of Utah
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Unpublished (2000)
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High quality sequence stop: 19.
Location/Qualifiers
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Insert Length: 10000 Std Error: (
Plate: 0109 row: I column: 13
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared NNA was blunt end-repaired with T4 NNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMs42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent 8. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                     AUTHORS
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                  AZ513919 19 bp DNA linear GSS 05-OCT-201100360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0360E13 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center University of Utah
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Contact: Robert
Mouse whole genome scaffolding with paired end reads from 10kb
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Similarity 94.7%;
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/strain="C578L/6J"
/db_xref="taxon:10090"
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Pred. No. 4.6e+02;
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FEATURES
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Best Local Similarity
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                  AZ645841 19 bp DNA linear GSS 14-DEC-200
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clone UUGC1M0511G04 R,
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Insert Length: 10000 Std Erro
Plate: 0360 row: E column: 1
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Fax: 801 585 7177
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/note="Vector: PWD42nv; Purified genomic
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Pred. No. 4.
genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb

Murinae; Mus.

GSS.

AZ645841

Mus musculus

Mus musculus (house mouse) AZ645841.1 GI:11775726

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REFERENCE
AUTHORS
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ORGANISM
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Best Local :
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Reseau
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                              Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.
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Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ende
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                         AZ650252 19 bp DNA linear GSS 1. 1M0520N17F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0520N17 F, genomic survey sequence.
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Location/Qualifiers
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_1lb="Mouse_10kb_plasmid_UUGCLM_1lbrary"
/note="Vector: PWD42nv, Purified_genomic_DNA_from_M.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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JOURNAL COMMENT
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RESULT 1000
AZ654747
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Best Local Similarity
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                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 19)
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19 bp DNA linear GSS 14-DEC-200
1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529F08 F, genomic survey sequence.
plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Erro
Plate: 0520 row: N column: 1
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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High quality sequence stop: 19.
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Fax: 801 585 7177
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/strain="C57BL/6J"
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m: 17
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Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea
                                                                                                                     1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                         Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0529 row: F column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF297010 20 bp mRNA linear EST 14-AUG-
30DGS--07-J24.bl Rice leaf plasmid CDNA library I (30DGS) Oryza
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Fax: 801 585 7177
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Location/Qualifiers
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 [gb] AF129072 l), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0529F08"
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/strain="C57BL/6J"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF333052 20 bp mRNA linear EST 18-AUG-2003
JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-M17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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CF333052.1 GI:33814360
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
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82 31 321 6355
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/lab host="E.coli DHIOB"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone Tib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                           /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                        /dev_stage="14 days after germination"
/lab_host="E.coli DHIOB"
/clome lib="AktWMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                      /db_xref="taxon:4530"
/clone="JMT--01-M17"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                            organism="Oryza sativa"
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Score 17.4; DB 1
Pred. No. 5.2e+02
0; Mismatches
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Pred. No. 5.2e+02;
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                                     DB 1;
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                                   Length 20
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AZ307896
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                    Query Match
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  Matches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0010 row: N column: 18
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ307896 22 bp DNA linear GSS 29-SEP-20010010N18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0010N18 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 22.
Location/Qualifiers
                                                                                                                         Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 [gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
Chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pMp42nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                             and selected for ampicillin resistance."
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0010N18"
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0; Mismatches
                         Score 17.4; DB 1;
Pred. No. 6.4e+02;
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                                                 Length 22;
Indels
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4463 CTTTTTTTTTTTTTTTT 4481

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4470 TITTTTTTTTTTTTTGTCTT 4488

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Conservative

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ed. No. 6.40 Mismatches

6.4e+02;

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Matches 18
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Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
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Location/Qualifiers
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Insert Length: 10000 Std Ercor: (
Plate: 0145 row: J column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                   Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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                                                    Score 17.4; DB 1;
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RESULT 1005
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Contact: Robert B.
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Class: plasmid ends
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Insert Length: 10000 Std Erro
Plate: 0222 row: P column: 09
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Fax: 801 585 7177
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clone UUGC1M0222P09 R, genomic survey sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMP42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance "
                                                                                                                                                                               Conservative
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                Score 17.4; DB 1;
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                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0169 row: N column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT
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  Conservative
                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNP42 (gi 4732114 |gb AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PW962nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mor_cype="genomic DNA"
/strain="C57BL/6J"
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/mol_type="qenomic DNA"
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/clone="UUGC2M0169N18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="Male"
                     0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiss
0;
                       Score 17.4;
Pred. No. 7e
  Mismatches
                          7e+02;
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KEYWORDS
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AZ399663
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                                         4466
σ
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Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: C column: 10
Seg primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 24.
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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TTTTGTTTTTTTTTTG 24
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                                                                                 Conservative
                                                                                                                                                     / Tab host="E. Coli strain XL10-Gold, T1-resistant, F-"
//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
//clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oilgonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWm42 (gil473214|gb)AF122072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UUGC1M0165C10"
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                                                                                                   Score 17.4; DB 1; Length 24; Pred. No. 7.7e+02;
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SOURCE
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AU265518
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CF319499
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                                                                               TITLE
                                                                                                                                                                                    ORGANISM
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                                                                                                                         AUTHORS
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AU265518
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Query Match
Best Local Similarity
                   Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 26)
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                              AU265518.1
EST.
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AU265518 VS
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--10-A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="0sHDACl-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived
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Tsukuba, Ibaraki 305-8572, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 bp mRNA linear EST 10-MAY-2002 discoideum cDNA clone VSF623 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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2M0087015R Mouse 10kb plasmid UT
clone UUGC2M0087015 R, genomic s
AZ818035
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0087 row: O column: 1:
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                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 26.
Location/Qualifiers
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid_UUGCIM_library"
/note="Vector: pMpd2nv; Purified genomic_DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0087015"
                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="AX4"
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                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="VSF623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Dictyostelium discoideum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:44689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
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UUGC1M library Mus musculus genomic
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                     polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
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Score 17.4; DB 1; Pred. No. 9e+02;

Length 26,

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JOURNAL COMMENT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0099 row: D column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were
                                                                                                              musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, /clone lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from I
                                                                                                                                                                                                                                                                                       organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                              clone="UUGC2M0099D17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ836072.1 GI:13005980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 28.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                /lab hoste "E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC2M0130K08"
                                                                                                                                                                                                                                                                                               'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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COMMENT

TITLE

DEFINITION CF299716/c RESULT 1014

CF299716 30 bp mRNA linear 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II

EST 15-AUG-2003 (7LEAF) Oryza

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SOURCE
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CF328476
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                                                                   Best Local
Matches :
                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 29)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF328476

29 bp mRNA linear EST NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-G12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongji, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                          Similarity
                                                                   Conservative
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                                                                                                                                                           /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days'
/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWp42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Oryza sativa"
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                                                              Score 17.4; DB 1; Length 29; Pred. No. 1.1e+03; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 bp mRNA linear E012712-024-017-115-T7 MPIZ-ADIS-024-storage root cDNA clone 024-017-I15 3-PRIME, mRNA sequence. BQ591372
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                                                                  ADIS DNA core facility at MPIZ
Max-Planck:Institute for Plant Breeding Research
                                                                                                                                                                               Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                         Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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CF299716.1 GI:33671477
                       Carl-von-Linne Weg 10, 50829 Koeln, Fax: 00492215062851
                                                                                                                 Contact: Weisshaar B
                                                                                                                                                                                                                                                                      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., 
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ591372.1 GI:26120955
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Location/Qualifiers
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                                                                                                                                         12472698
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82 31 321 6355
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weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="7 days after germination"
/lab_host="8.coli DNIOS"
/lab_host="8.coli DNIOS"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon.4530"
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Matches
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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HD--08-E17.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-E17, mRNA sequence.
                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                            of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAGAAAAAAAAAAAA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                       bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung, Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SAI; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: SAI; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saitzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      /clone lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prof. Christian Jung; Sequence submission manaç
RZPD/GABI-Primary database: http://gabi.rzpd.de
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                                                           /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E_coli_DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="storage root"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-I15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
/note="Vector: pCR4-TOPO; Site_1:
                                                                                                                                    'clone="HD--08-E17"
                                                                                                                                                                                                                                                              ocation/Qualifiers
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Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                     bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                         GreenGene Biotech Inc.; Division , MyongJi University
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    EcoRI; Callus was
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FEATURES
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BQ591193
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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32
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E012715-024-017-D14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-D14 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carl-von-Linne Weg 10, 50829 Koeln, Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Max-Planck-Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADIS DNA core facility at MPIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 22)
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primer: T7; GTAATACGACTCACTATAGGGC
                                            Conservative
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Length: 22 Std Error: 0.
                                                                                                                                                                                                                                                                             /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                  Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schmeider, coordinator: Prof. Christian Jung, Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de*
                                                                                                                                                                                                          SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet
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                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:161934"
/clone="024-017-D14"
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                                            0; Mismatches
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                                                                  Score 17.2; DB 1;
Pred. No. 6.9e+02;
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                                                                                      Length 22;
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Query Match Best Local S Matches 19

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0.2%; larity 86.4%; Conservative

Pred. No. 6.9 ); Mismatches Score 17.2;

6.9e+02

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DB 1; Length 22;

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SOURCE
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AZ442146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0234 row: B column: 10
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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1M0234B16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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Imboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND2 (gi|4732114|gb|AFT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vetor: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="UUGC1M0234B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
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                                                                                          AZ382429/c
                                                                                                                        RESULT 1020
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Best Local Similarity
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Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LIMI) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/simage.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 23 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM10 row: O column: 3
                                                                                                                                                                                                                                                AZ382429 23 bp DNA lineat 1M0139E11R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0139E11 R, genomic survey sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Other_ESTs: 2823002.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW245956.1 GI:6588949
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2823002.3prime
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
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                                                                                                                                                                                                                                                                                                                              Conservative
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/lab host="DH108 (phage-resistant)"
/clome lib="NIH MGC 7"
/clome lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:2823002"
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Pred. No. 7.6e+02;
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                              musculus genomic
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DEFINITION

AZ447220 23 bp DNA linear GSS 04-OCT-200 1M0244E15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244E15 F, genomic survey sequence.

GSS 04-OCT-2000

ACCESSION

RESULT 1021

AZ447220/c

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SOURCE
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                                                                                         Local Similarity
19;
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AZ382429.1 GI:10496129
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: E column: 11
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                 Conservative
                                                                                                                                                           http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                         Score 17.2; DB 1;
Pred. No. 7.6e+02;
                                                                    Mismatches
                                                                                                                  DB 1; Length 23;
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Matches 19; Conserv
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AU257964 3'-directed mouse cDNA library Mus
BED0011649 3', mRNA sequence.
AU257964
AU257964.1 GI:20323086
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Insert Length: 10000 Std Error:
Plate: 0244 row: E column: 15
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Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (
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GSS.
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0244E15"
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                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0008 row: G column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Niederhausern, B. and Wright, D., Weiss, R. Nouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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24 bp DNA linear GSS 29-SEP-20
1M0008G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0008G01 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
                                                                                 High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
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AZ307138.1 GI:10345841
                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kkato@bs.aist-nara.ac.jp/
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Pred. No. 8.3e+02;
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Best Local
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                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ514388 24 bp DNA linear GSS 05-OCT-20
1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0361H04 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center University of Utah
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                                                                                                                                                               High quality sequence stop: 24.
                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
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Similarity 86.4%;
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                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                     Location/Qualifiers
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xref="taxon:10090"
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Pred. No. 8.3e+02;
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Sciurognathi; Muridae; Murinae; Mus.
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AZ814317/c
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ORGANISM
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                High quality sequence stop: 24.
                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0082 row: C column: 12
Seq primer: CGTTGTAAAACGACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2M0082C12F Mouse 10kb plasmid UUGC1M library Mu clone UUGC2M0082C12 F, genomic survey sequence.
                                                                                                                                                                                           Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                USA
                      /mol_type="genomic_DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XL10-Gold, T1-resistant,
/clome_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
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                                                                                       organism="Mus musculus"
/clone="UUGC2M0082C12"
                                                                                                                                            ocation/Qualifiers
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Pred. No. 8.
                                                                                                                                                                                                                                                            Std Error: 0.00
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RESULT 1026
AW247153
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                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center

Trimming: cross match from University of Washingtion Genome Center

PHRAP suite. PoTy-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project: University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 7 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 25 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

beginning of the sequence, this cDNA insert was polyadenylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Other_ESTs: 2819969.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWZ47153 25 bp mRNA linear EST 07-JAN-2000
2819969.3prime NIH_MGC_7 Homo Bapiens cDNA clone IMAGE:2819969 3',
                                                                                                                                                          Plate: LLCM2 row: P column: 18 High quality sequence stop: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                   Location/Qualifiers
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Pred. No. 8.3e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0084 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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/clone="MAGE:2819969"
/tissue_type="small_cell_carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/clone_tib="NIH_MGC 7"
/cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                      /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                clone="UUGC1M0084G04"
                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
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Pred. No. 9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Std Error: 0.
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9e+02;
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RESULT 1028
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Matches 19
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At2g45650. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P. Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC883604.1 GI:33359960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ecker@salk.edu
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                              /clone="SALK 095121.17.80.n"
/clone=lib="Arabidopsis thallana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thallana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|strain="Columbia_0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               db xref="taxon:3702"
                          86.4%;
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                       0.2%; Score 17.2; DB 1; Length 25; 86.4%; Pred. No. 9e+02;
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Pred. No. 9e+02;
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VERSION KEYWORDS

ACCESSION

REFERENCE

AUTHORS

FEATURES

COMMENT

JOURNAL TITLE 밁 ફ

Matches

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RESULT 1029
BG865511
LOCUS
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                      VERSION
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BG292912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4012 AAAATGAGAAAAAGAGAGAAAACAAAATG 4041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 האוא פון טיט עם mkNA linear EST 29-MAY-2001 602783643F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909811 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Email: cgapbs-r@mail.nih.gov
                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 31)
                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                    TST
                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                   602389549F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4501164 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10809 row: e column: 12 High quality sequence stop: 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 30)
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                                                                                                                                                                                                                                      BG292912.1 GI:13052227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="IMAGE:4909811"
/clone="IMAGE:4909811"
/lab host="PHIOB (TI phage-resistant)"
/clone_lib="NCI CGAP_SG2"
/clone_lib="NCI CGAP_SG2"
/note="Torgan: salivary gland; Vector: pCMV-SPORT6; Site_/note="Torgan: salivary gland; Vector: pCMV-SPORT6; Site_NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oli MT. Average insert size 1.3 kb. Constructed by Life dT. Average insert size 1.3 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Technologies. Note: this is a NCI_CGAP Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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EST.
                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, of Bioscience and Bioinformatics, Yongin, Kyeonggi, Korea
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF302459 32 bp mRNA linea 7LEAF--08-A01.gl Rice leaf plasmid cDNA library sativa cDNA clone 7LEAF--08-A01, mRNA sequence.
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plate: LLAM10368 row: b column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
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Location/Qualifiers
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/clone lib="NIH_MGC 94"
/clone lib="NIH_MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Site 2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                        /clone="7LEAF--08-A01"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA_was_cappe
/....e="vector: pck4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for pr.orp "
                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xxef="taxoni4530"
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Pred. No. 1.3e+03;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                     bhnahm@bio.myongji.ac.kr
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, MyongJi University
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brary II (7LEAF) Oryza
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Nouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 26td Error: (
Plate: 0367 row: C column: 12
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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32 bp DNA linear GSS 13-DEC-20
1M0367C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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gh quality sequence stop: 32.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM042 (gi[4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0367C12"
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     Contract: Nahm B.H.

Contract: Nahm B.H.

Genomics and Genetics Institute, Greendene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeenggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Linchmahla micropii an kr
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                               Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                             CF302250
CF302250.1 GI:33674011
                                                                                                                                                                                                                                                                                                                                                                  CF302250 34 bp mRNA linear EST 15-AUG-2003 7LEAF--07-J10.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-J10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygil; Neopterygil; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 32)
Humphray, S.J., Huckle, E. and Hunt, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-UN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio genomic clone
AL735323
 Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Further details: http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Similarity 73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-1F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="vector pindigoBAC-536"
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Pred. No. 1.3e+03;
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bhnahm@bio.myongji.ac.kr
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Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
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Best Local S
Matches 22
                                                                                                                           Query Match
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22; Conserv
  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            b', mRNA sequence.
BF338797
                                                                                  Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35)
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602036229F1 NCI_CGAP_Brn64 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: pLAM9501 row: j column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF338797.1
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                                        AAAATGAGAAAAAGAGAGAAAACAAAATG 4041
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                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mtNA"
/mol_type="mtNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:4184167"
/tissue_type="glioblastoma with EGFR amplification"
/tissue_type="glioblastoma with EGFR amplification"
/tlab host="MHIOB (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/clone_lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/cultivar="Nackdong"
/db xref="taxon:4330"
/db xref="taxon:4330"
/clone="TERF-07-710"
/tissue type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Nation" | DCR4-TOPO; Site 1: EcoRI; mRNA was capped
/note="Vector: pCR4-TOPO; Site 1: Book as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was cap
with oligoribonucleotides and then used as templates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/mol_type="mRNA"
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Pred. No. 1.4e+03;
0; Mismatches 8;
                                                                                                         Score 17.2; DB 1;
Pred. No. 1.5e+03;
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                                                                                                                             DB 1;
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                                                                                                                             Length 35;
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RESULT 1037
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MEDLINE
PUBMED
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Best Local
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                                                                                                                  BQ591177 17 bp mRNA linear EST 06-DEC-2
E012715-024-017-B22-T7 MPIZ-ADIS-024-Storage root Beta vulgaris
cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
                             BQ591177
BQ591177.1 GI:26120760
EST.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophylales; Amaranthaceae; Beta.
1 (bases 1 to 17)
1 (bases 1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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17 bp mRNA linear EST 06-DEC-:
S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
BQ590687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ590687.1 GI:26120270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il: weisshaa@mpiz-koeln.mpg.de
ert Length: 17 Std Error: 0.00
te: 18 row: B column: 24
primer: T7; GTAATACGACTCACTATAGGGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Salf, Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage_root"
/lab_host="EMDH10B"
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100.0%; Pred. No. 4.2e+0
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hes 0;
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Query Match
Best Local Similarity
                                                                                                                        Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoldeae; Oryzeae; Oryza.
1 (bases 1 to 17)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                  14ROOT--01-A21.b1 Rice root plasmid cDNA library sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                     CF290854.1 GI:33659887
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Plate: 17 row: B column: 22
Seq primer: T7; GTANTACGACTCACTATAGGGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: weisshaa@mpiz-koeln.mpg.de
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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/clone="024-017-B22"
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/mol_type="mRNA"
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/lab_host="EMDH10B"
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100.0%; Pred. No. 4.2e+02;
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                                                                                                                                                        Poaceae;
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myong'I University Yongin, Kyeongyi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice BSTs
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF295807 17 bp mRNA linear EST 14-AUG-30DGS--05-012.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-012, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
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Location/Qualifiers
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                                                                                        /culTivar="Nackdong"
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/db xref="taxon:4530"
/clone="3005S--05-012"
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/tissue_type="leaf"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
RT-PCR."
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/dev_stage="14 days after
/dev_stage="15 days after
/lab_host="E.coli DH108"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--01-A21"
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|mol_type="mRNA"
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  Score 17; DB
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1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                 Oryza sativa
Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                               CF299639 17 bp mRNA linear TLEAF-03-L20.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--03-L20, mRNA sequence. CF299639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbbo.com, bhna
Location/Qualifiers
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                                                                                                                                                                                    Oryza sativa
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                                                                                                                                                                                                                              CF299639.1 GI:33671400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:4530"
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/clone="7LEAF-02-A18"
/tissue_type="leaf"
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/lab host="E.coli DHIOB"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-pCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/mol_type="mRNA"
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Pred. No. 4.2e+0
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                                                               Kim, M.J., Lee, T.H.,
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(7LEAF) Oryza
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(7LEAF) Oryza
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REFERENCE
AUTHORS
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CF310219
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ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABF--04-M02.gl ABF3-overexpressing transgenic rice
library (ABF) Oryza sativa cDNA clone ABF--04-M02,
CF310219
CF310219.1 GI:33681980
                                                                                                                                                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF310219
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
                                                                                                                                                                     /cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-M02"
/tissue_type="leaf"
                 /clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

(DNA library (ABF)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for pCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4530"
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/tissue_type="leaf"
/tissue_type="leaf"
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/clone 11b="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                             /organism="Oryza sativa"
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                                                                                                                                  /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No.
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rice plasmid cDNA
-M02, mRNA sequence.
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AL048754/c
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VERSION
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LOCUS
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Best Local (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      Homo sapiens
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Query Match 0.2%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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                                                                       DKFZp566L173 rl 566 (synonym: DKFZp566L173, mRNA sequence.
                                      AL048754
AL048754.1
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Oryza sativa
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                         methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library (JMT) "
                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="leaf"
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/lab_host="E.coli_DH108"
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                                        GI:4727825
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
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                                                                                             18 bp mRNA
ym: hfkd2) Homo
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REFERENCE
AUTHORS
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CF301057
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Best Local
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                                  l Similarity
17; Conserv
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
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18 bp mRNA linear EST 15-7LEAF--05-M05.bl Rice leaf plasmid cDNA library II (7LEAF) sativa cDNA clone 7LEAF--05-M05, mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
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                                  Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                      bhnahm@ggbio.com,
                                                                                                    /db xref="taxon:4530"
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/clone="7LEAF--05-M05"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="kidney"
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/lab host="X1-2blue"
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/note="Vector: pamPl; Site_1: NotI; Site_2: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                     0.2%;
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                                Score 17; DB
Pred. No. 4.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        bhnahm@bio.myongji.ac.kr
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, 4.8e+02;
:hes 0; Indels
                                  4.8e+02;
hes 0;
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                                                                   Length 18;
                                    Indels
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Best Local S
Matches 17
                                      TITLE
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                                                                                                      AUTHORS
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            1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                            NACL--02-C04.bl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-C04, mRNA sequence.
                                                                                                                                      Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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17; Conserv
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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  Genomics
                                                                                                                                                                                                                            Oryza sativa
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    Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
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with_oligoribonucleotides and then used as templates for
RT-PCR."
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and Genetics Institute,
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Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
  GreenGene Biotech Inc.; Division
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AZ345795/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0080 row: H column: 09
                                                                                                                                                                                                                                                                                                                                                                                          84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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Seq primer: CACACAGGAAACAGCTATGACC
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Unpublished (20)
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AZ345795.1 GI:10425032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                           ass: plasmid ends
                                                                                                                                                                                                                                quality sequence stop: 19.
Location/Qualifiers
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82 31 330 6193
82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg.,
                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0080H09"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                         sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                               0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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ACCESSION
VERSION
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SOURCE
ORGANISM
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AZ650575/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0520 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                            Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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19 bp DNA linear GSS 14-DEC-200
1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0520P13 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ650575.1 GI:11785200
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse_10kb_plasmid_UUGC1M_library" /note="Vector: PW042nv, Furified_genomic_DNA_from_Nosculus_C578L/6J (male) was obtained_from_the_Jac_
                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained
                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                    sex="Male"
                                                                                                                            clone="UUGC1M0520P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 1;
Pred. No. 5.4e+(
                                                                                                                                                                                                                                                                                                                                                                                                           Std Error: 0.00
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from M.
che Jackson
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RESULT 1050
AZ853220/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0156 row: J column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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19 bp DNA linear GSS 21-FEB-200
2M0156J15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0156J15 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0156J15"
                                                                                                                                   sex="Male"
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VERSION KEYWORDS

ACCESSION

REFERENCE

AUTHORS

COMMENT

JOURNAL

TITLE

COMMENT

TITLE

FEATURES

Laboratory Mouse DNA Resource

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FEATURES
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                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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17; Conserv
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF298018

7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-D19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF298018.1 GI:33669779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi,
                           TTTTTTTTTTTTTTG 4484
TTTTTTTTTTTTTTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                             Conservative
                                                                                                                                                                                                       /organism="Oryza sativa"
/mol type="mRNA"
/mol type="mRNA"
/cultivat="Nackdong"
/cultivat="Nackdong"
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/dev_stage="7 days after germination"
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/lab host="E.coli DHIOB"
/clone_Tib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_Tib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                 0.2%;
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Pred. No.
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Pred. No.
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. 6e+02;
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)
                                                                                                                                                                                                                                    AZ818055.1 GI:12987963
GSS.
                                                                                                                                                                                                                                                                                              2M0087B23R Mouse 10kb plasmid UUGCIM library Mucline UUGC2M0087B23 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Oryza sativa
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20 bp mRNA linear EST 15-AUG-2003
HD--09-020.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-020, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF319428.1 GI:33691189
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4530"
/clone="HD--09-020"
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100.0%; Pred. No. 6e+02;
ive 0; Mismatches 0; Indels
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UUGC1M library Mus musculus genomic
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                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21)
1 (bases 1 to 21)
1 (berrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                   DKFZp566N143 r1 566 (synonym: DKFZp566N143, mRNA sequence.
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Contact: Robert B.
Ingolstaedter Landstr.1, D-8
                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                              AL048772.1 GI:4727843
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Insert Length: 10000 Scd Error: (
Plate: 0087 row: B column: 23
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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gh quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
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/mol_type="genomic מאים"
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/clone="UUGC2M0087B23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddurn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0436 row: G column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
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AZ610868.1 GI:11733058
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801 585 7177
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/mol_type="maNA"
/db_xref="taxon:9606"
/clone="DKFZp566N143"
/tissue_type="kidney"
/tissue_type="fetal"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                           /lab host "B. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pM042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                   sex="Male
                                                                                                                                                                                                                                                                                                                        clone="UUGC1M0436G12"
                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
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AZ764492/c
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0560 row: D column: 04
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1M0560D04R Mouse 10kb plasmid clone UUGC1M0560D04 R, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The sassage through was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse_10kb_plasmid_UUGC1M_library" /note="Vector: pW042Tuv, Purified_genomic_DNA_from_M.musculus_C57BL/6J (male) was obtained_from_the_Jackson_
                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                       'sex="Male"
                                                                                                                                                                                                                                                                                                                         clone="UUGC1M0560D04"
                                                                                                                                                                                                                                                                                                                                                        db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                          mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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kb range using preparative agarose gel

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RESULT 1058
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Matches 17; Conserv
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                                                                                                                                                        4463 CTTTTTTTTTTTTTT 4479
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF310806 22 bp mRNA linear EST 15-AUG-2003 ABF--05-K20.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-K20, mRNA sequence.
  AZ310057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                      /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_nost="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA lībrary (ABF)"
cDNA lībrary (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:4530"
'clone="ABF--05-K20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 7.4e+02;
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RESULT 1059 BX550903

DEFINITION

BX550903

Glossina morsitans morsitans adult infected

mRNA

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KEYWORDS
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17; Conserv
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018A15 R, genomic survey sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0018 row: A column: 15
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 22)
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Fax: 801 585 7177
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                                                                                               Conservative
                                                                                                                                                                                      Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                               0.2%; Score 17; DB 1;
100.0%; Pred. No. 7.4e+0
tive 0; Mismatches
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                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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Glossina morsitans morsitans
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Bangor LL57 2UW
All clones with suff
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
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Contact: Hall N
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Genome Biol. 4 (10), R63 (2003)
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EST.
                plasmid inserts
Unpublished (2000)
                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         morsitans morsitans and expression analysis of putative immune
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  Contact: Robert
                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                    AZ448207.1 GI:10600777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Tsel15e01 q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="country: Zimbabwe; EST from adult gut infected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="morsitans"
/db_xref="taxon:37546"
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100.0%; Pred. No. 8.1e+02;
htive 0; Mismatches 0;
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RESULT 1061
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17; Conserv
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1 (bases 1 to 25)

1 (rushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda, Makeuchi,I., Kohara,Y. and Tanaka,Y.

Population analysis of CDNAs from unicellular and multicellular stages of Dictyostelium discoideum

Unpublished (2002)
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AU268810 VS Dictyostelium
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Insert Length: 10000 Std Error: (
Plate: 0245 row: E column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Tel: 81-298-53-4664
                                                              Institute of Biological Sciences
University of Tsukuba
                                                                                                                                             Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum Dictyostelium discoideum
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Fax: 801 585 7177
                                 -1-1 Tennoudai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
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                                 Tsukuba, Ibaraki 305-8572, Japan
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Best Local S
Matches 20
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TITLE
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                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strainberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center:

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

PHRAP suite. Toly-T Identification: patMatch.pl from Berkeley

PHRAP suite. Toly-T Identification: patMatch.pl from Berkeley

PHRAP suite. Toly-Sequence. Trace file contained 25 contiguous distinct peaks

following vector sequence. Very Low

Quality Sequence: Trace file contained 25 contiguous distinct peaks

following vector sequence. Poly-Medenylation: Based upon the presence

of a xhoi site followed by a run of 14 or more T residues at the

beginning of the sequence, this cDNA insert was polyadenylated.

Incarton/Onlification: A column: 21.
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Other_ESTs: 2819996.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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2819996.3prime NIH_MGC_7 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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/lab host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_7"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:281996"
                                                                                                                                                                         /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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/clone_lib="VS"
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/clone="VSI514"
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; Pred. No. 9.6e
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                                                                CF300714 25 bp mRNA linear EST 15-AUG-2003 7LEAF--05-E19.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-E19, mRNA sequence. CF300714
EST.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 25)

Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.

The pattern of gene expression in human hematopoietic CD34+
stem(progenitor cells
Unpublished (2001)
                                           CF300714.1 GI:33672475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: swangl@midway.uchicago.edu
This EST fragment was amplified from cDNA Library of human CD 34+
stem/progenitor cells with GLGI technique (Generation of Longer
cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
the first CATG site of the target cDNA sequence.
Seq primer: M13 Forward.
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EST-CD34N-028 cDNA library of human CD
Homo sapiens cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Chicago Medical Center 5841 S. Maryland Ave., MC2115, Chicago, Tel: 773-702-6788

Fax: 773-702-3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Bone marrow"
/cell_type="CD34+ stem/progenitor cells"
/clone_lib="CDNA library of human CD 34+ stem/progenitor cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologic
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="3'ESTs converted from the SAGE tag
GLGI method"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

I.arge-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 25)
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF315032 25 bp mRNA linear EST 15-AUG-2003 HD--03-M19.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--03-M19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
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Unpublished (2003)
                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
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Unpublished (2003)
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82 31 321 6355
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Location/Qualifiers
                                                                                                                                                     bhnahm@ggbio.com,
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                            organism="Oryza sativa"
ool_type="mRNA"
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one="HD--03-M19"
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Pred. No. 9.6e+02;
0; Mismatches 5
                                                                                                                                                     bhnahm@bio.myongji.ac.kr
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Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymer
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 25.
Location/Qualifiers
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0536 row: E column: 18
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                        /lab host="B. Coli strain XL10-Gold, T1-resistant, F-"/clome_lib="Mouse 10kb plasmid UUGCIM library./note="Vector: PW9A2nv; Purified genomic DNA from M./note="Vector: PW9A2nv; Burified genomic DNA from M./note="Vector: PW9A2nv; Mas obtained from the Jacksomusculus C57BL/6J (male) was obtained fro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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lab_host="B.coli DH10B"
                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC1M0536E18"
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Pred. No.
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kb range using preparative agarose gel

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RESULT 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TA12F02Q
T. brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harrie,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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AL451366.1 GI:11833388
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brucei sheared genomic DNA clone 12f02, reverse sequence,
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                                                                                                                                                                                                                                                                                                                                               /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                             /clone="12f02"
                    26 bp mRNA linear EST Dictyostelium discoideum cDNA clone VSF805
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100.0%; Pred. No.
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805 5', mRNA
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1 (bases 1 to 26)

Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, N. Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multicellular
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                                                                                                                                                                                            1-1-1 Tennoudai, Tsu
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                              stages of Dictyostelium discoideum Unpublished (2002)
Contact: Hideko Urushihara
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Contact: Hideko Urushihara
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Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
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Dictyostelium discoideum
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 26)
                                                                                                                                                                                                                                             University of Tsukuba
                                                                                                                                                                                                                                                               Institute of Biological Sciences
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Location/Qualifiers
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Fax: 81-298-53-6614
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AU265818.1
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                                                                                                                                                                          hideko@biol.tsukuba.ac.jp
                                                                                     /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
                                                      /db_xref="taxon:44689"
/clone="VSI294"
dev_stage="vegetative"
clone_lib="VS"
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/clone_lib="VS"
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/strain="AX4"
                                      sex="mat A"
                                                                                                                                                          ocation/Qualifiers
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clone="VSF805"
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Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; S
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: O column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 26.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of phm42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pW042nv, purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0105007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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Pred. No. 1e+03;
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
1 (bases 1 to 30)
Humphray, S.J., Huckle, E. and Hunt, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 28)
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I.,
Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA852828 28 bp mRNA linear EST 20-JUN-2002
NHTBCae16e07f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
                                                                                                                                      AL987581.1 GI:25176586
GSS.
                                                                                                                                                                                         DR31A15T 30 bp DN Danio rerio genomic clone DKEY-31A15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: libin@helix.nih.gov
Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Libin Jia
Medical Genetics Branch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone NHTBCae16e07, mRNA sequence.
                                                                                                                  Danio rerio (zebrafish)
                                                                                                                                                                          AL987581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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10/10C101, 9000 Rockville Pike, Bethesda,
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Hip; Vector: pBluescript; Site 1:
Library constructed by Dr. Marian Young and Dr.
Gehron Robey (NIDCR)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="Bone"
/cell type="Trabecular Bone Cells"
/lab_host="SURE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="NHTBCae16e07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Pred. No.
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Pred. No. 1.2e+03;
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AW245279/c
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                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: O contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 31 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Floration/Onalificars

Plate: LCM3 row: C column: 21.
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1 (Dases 1 to 31)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 31A15. 31A15 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
'cell line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_
                                                                                             /clone="IMAGE:2820044"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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76.9%;
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Pred. No. 1.3e+03;
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Query Match Best Local S Matches 23

Local S. 23; 4007

Similarity

0.2%;

Score 17; DB 1; Pred. No. 1.5e+03; D; Mismatches 1(

10;

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Gaps

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Length 34;

Conservative

GGTCTAAAATGAGAAAAAAGAGAGAAAACAAAA 4039

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JOURNAL COMMENT
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AUTHORS
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ORGANISM
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BG531309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLCM1526 row: e column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                 /tissue_type="embryonal carcinoma"
/lab host="bH108 (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/clone_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/sfi (ggccgcctcggcc); Site_2: Sfi (ggccattatggcc);
/sfi (ggccgccattatggcc); Site_2: Sfi (ggccattatggcc);
/and 3 adaptors were used in cloning as follows: 5
/adaptor sequence: 5'-CACGGCCATTANGGCC-3' and 3' adaptor
/sequence: 5'-ATTCTAGAGGCCGAGGCGGCAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
/sontained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:4697459"
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Pred. No. 1.4e+03;
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SOURCE
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BX567522/c
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MEDLINE
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        AUTHORS
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1 (bases 1 to 37)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3/ pp mRNA linear EST 14-OCT-2003 BX567522 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse88e03_plc, mRNA sequence.
                                            Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                           20 bp mRNA linear EST 15-AUG-207LEAF--05-K03.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-K03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
      1 (bases Kim, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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                                                                                                                              Oryza sativa
                                                                                                                                                                       CF300961.1 GI:33672722
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rhartoideae; Oryzeae; Oryza.
(bases 1 to 20)
m,J.S., Jun,K.M., Cheong,P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clones with suffix qlc are reverse primer reads starting at of the cDNA all plc reads are from
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="country: Zimbabwe;
T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="Tse88e03_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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Pred. No. 1.6e-
0; Mismatches
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    Kim, M.J.,
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    Lee, T.H., Shin, Y.C.,
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CF301101
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Best Local Similarity 90.0%;
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Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute,
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/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="71EaF--05-N04"
/tissue_type="leaf"
/dev stage="7 days after germination"
/dev stage="7 days after germination"
/lab hoste="E.coli DH10B"
/clone_1b="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                               bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--05-K03"
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/dev_stage="7 days after germination"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone lib="Nace leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                      GreenGene Biotech Inc.; Division
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CF336815
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Best Local S
Matches 18
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                           AZ343730 20 bp
1M0077E20F Mouse 10kb plasmid Ut
clone UUGC1M0077E20 F, genomic E
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                         Mus musculus (house mouse)
                                                                            AZ343730.1 GI:10422288 GSS.
                                                                                                                 AZ343730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJI University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JMT--07-A04.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence. CF336815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--07-A04"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf"
/dev_gtage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 1; Pred. No. 6.5e+02;
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Pred. No. 6.5e+02;
                                                                                                                            genomic survey sequence.
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                                                                                                                                             bp DNA linear GSS 29-SEP-2000
UUGC1M library Mus musculus genomic
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          20 bp DNA linear GSS 29-SEP-200 IMO081P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0081P11 F, genomic survey sequence.
AZ346143
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 20)
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                                                                                                                              Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                       AZ346143.1 GI:10425380
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Unpublished (2000)
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Insert Length: 10000 Std Error:
Plate: 0077 row: E column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome
University of Utah
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
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/clone="UUGC1M0077E20"
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/strain="C57BL/6J"
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Pred. No. 6.5e+02;
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Nouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                AZ633741
20 bp DNA TIME 1M0489G12F Mouse 10kb plasmid UUGCIM library Mu clone UUGC1M0489G12 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: P column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)
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Dunn, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus C57BL/6U (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH22 (gi |4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells
Aoyagi, A., Barber, M.,
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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strain="C57BL/6J"
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Beacorn, T., Duval, B., Hamil, C.,
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 21) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Insert Length: 10000 Std Error:
Plate: 0489 row: G column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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Pax: 801 585 7177
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Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                              AW248782.1 GI:6591775
                                                                                                                                                                                                                                        mRNA sequence.
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0.005 inch orifice at constant velocity. The sheared DNA
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polymucleotide kinase. Adaptor oligonucleotides were
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adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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CF319122
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Best Local Similarity
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Tissue Procurement: DCTD/DTp cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center:
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patkmatch.pl from Berkeley
Drosophila Genome Project: University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases following vector sequence: Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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High quality sequence stop: 21.
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Contact: Robert Strausberg, Ph.D.
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ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/cell_line="MGC3"
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|mol_type="mRNA"
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he lib="NIH MGC 7"
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Pred. No. 7.3e+02;
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Kim, J.S., Dun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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HD--10-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid of
library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence
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Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com, bhna
Location/Qualifiers
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-D06"
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                                                                                                                               tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="B_coli_DH10B"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/lab_lib="OSHDAC1-overexpressing transgenic rice plasmid
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/cultivar="Nackdong"
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/mol_type="mRNA"
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/clone="HD--09-I07"
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Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                    bhnahm@bio.myongji.ac.kr
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1M0282004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0282004 F, genomic survey sequence
AZ468862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: O column: 04
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University of Utah Genome Center
University of Utah
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1 (bases 1 to 21)
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UUGC1M0282004"
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Pred. No. 7.3e+02;
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Query Match

0.2%;

Score 16.8;

DB 1;

Length 21;

Query Match Best Local Similarity

90.0%;

Score 16.8; DB 1; Pred. No. 7.3e+02;

Length 21;

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RESULT 1086
AZ597932
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AUTHORS
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Mouse whole genome scaffolding with paired end reads from 10kb
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1M0412D23F Mouse 10kb plasmid UUGC1M library Mu
clone UUGC1M0412D23 F, genomic survey sequence.
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0412 row: D column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GSS.
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Fax: 801 585 7177
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                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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     and selected
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/strain="C57BL/6J"
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for ampicillin resistance.
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UUGC1M library Mus musculus genomic
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     Query Match 0.2%;
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 race: 0514 row: I column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: I column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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Mus musculus (house mouse)
Mus musculus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84112, USA
Tel: 801 585 5606
Pax: 801 585 7177
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21 bp DNA linear GSS 14-DEC-200
1M0514I17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0514I17 F, genomic survey sequence.
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AZ647578.1 GI:11779183
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                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. col1 XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PW027nv, Dvrifted genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomedical Polymers Research Bldg.,
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/clone="UUGC1M0514I17"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
     Score 16.8; DB 1;
Pred. No. 7.3e+02;
0; Mismatches 2;
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                                                  Length 21;
     Indels
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AW246884
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AL Unpublished (1999)

Other_ESTs: 2822626.5prime
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Fissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage/inage.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch pl from Berkeley
Drosophila Genome Project: University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 20
contiguous PHRED high quality bases following vector sequence.
Plate: LLCM9 row: O column: 11
High quality sequence stop: 20.
S LLCM9 row: O column: 11
Location/Qualifiers
                                                       4463 CITTITITITITITITITI 4482
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1 (bases 1 to 22)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                     /lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8bb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2822626"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                    (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                90.0%;
                                                                                                           <u>.</u>
                                                                                                                                Score 16.8; DB 1; Length 22; Pred. No. 8e+02;
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AZ345485 LOCUS

RESULT 1089

DEFINITION

AZ345485 22 bp DNA linear GSS 29-SEP-20 1M0080CO2F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

GSS 29-SEP-2000

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Best Local Similarity
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AZ662734 23 bp DNA linear GSS 14 1M0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0542D04 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 02
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University of Utah Genome Center
University of Utah
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AZ345485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 bb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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clone="UUGC1M0080C02"
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Pred. No. 8e+02;
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                                                                                                                              RESULT 1091
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NACL--08-C13.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--08-C13, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0542 row: D column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
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AZ662734.1 GI:11799880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). Was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel elettrophoresis. Vector DNA was prepared from a derivative of phasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptors was annealed to adaptors were name and transformed into
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                                                                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/Clone_11b="Mouse 10kb plasmid UUGCIM 11brary"
/note="Vector: PW927v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 8.
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CF331868/c
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AUTHORS
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Matches 18
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                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NACL--08-C13.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-C13, mRNA sequence.
CF331868
CF331868.1 GI:33811959
EST.
                                                                                                                                                                                                                                                                       1 (bases 1 to 24)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 24)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                   Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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18; Conservative
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                                                                                         bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NACL--08-C13"
/tisue type="callus"
/tisue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/clone_tib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
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Pred No. 9.5e+02;
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punn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0022 row: L column: 22
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="NACL--08-C13"
/tissue_Type="callus"
/tissue_Type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_Tibe="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb plasmid_UUGCIM_library"/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_
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                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC2M0022L22"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:10090"
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kb range using preparative agarose gel

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Best Local :
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Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                       28 bp mRNA linear EST 14-AUG-20
14ETL--09-N05.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
CF282351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 25) Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K. Analysis of gene expression in mouse embryogenesis by 3'-directed chua seminoring.
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MUSGS00987 Mouse 3'-directed
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EST.
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Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kawamoto, S., Okubo, K., Yoshii, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mb1686 3', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="decidual tissue (day 6.5-8.5/clone_lib="Mouse 3'-directed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:10092"
/clone="mb1686"
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                                                                                                                                                                                                                               Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                               I (bases 1 to 28)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,JK., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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CF321885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HD--13-E16.g1 OsHDAC1-overexpressing transgenic rice plasmid cI
library (HD) Oryza sativa cDNA clone HD--13-E16, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF321885.1 GI:33693646
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                                                                                                                                                                                                                bhnahm@ggbio.com,
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                                                                           /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxxon:4530"
/clone="HD--13-E16"
/tissue_type="callus"
/dev_stage="proliferated callus on
/dev_stage="proliferated callus on
/lab_host="E, coli DH10B"
/clone_lib="OsHDAC1-overexpressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCR4-TOPO; with oligoribonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4530"
/clone="14ETL--09-N05"
                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                       Korea
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Pred. No. 1.2e+03
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                                                                                                                                                                                                              bhnahm@bio.myongji.ac.kr
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, MyongJi University
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                                         2N6
                                       media for 2 weeks"
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AUTHORS
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VERSION
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CF330938
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ORGANISM
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CF330748/c
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Best Local S
Matches 21
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JOURNAL
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CF330938 28 bp mRNA linear EST 18-AUG-2003 MACL-06-N19.gl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-N19, mRNA sequence.
CF330938 CF330938.1 GI:33810102
EST.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF330748 28 bp mRNA linear EST NACL--06-J14.gl Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--06-J14, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF330748.1 GI:33809717
EST.
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                                                                                                                                                                                                                                                                                            Similarity
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Location/Qualifiers
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derived
                                                                                                                                                                                                                                                                                                                                                   /clone="NACL--06-J14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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75.0%;
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Pred. No. 1.2e
0; Mismatches
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Pred. No. 1.2e
0; Mismatches
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AZ399637/c
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AUTHORS
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JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnægenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: N Column: 04
Seg primer: CACAAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ399637 28 bp DNA linear 100165N04R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0165N04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research
                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
Unpublished (2000)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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/mol_type="mRNA"
/mol_type="mRNA"
/culTivar="Nackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/clone="NACL-06-N19"
/clone="NACL-06-N19"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated
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Location/Qualifiers
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Pred. No. 1.2e+03;
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0168 row: O column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Nouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                  University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                  plasmid inserts
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/strain="C57BL/6J"
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1M0286K08R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0286K08 R, genomic survey semience
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                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0286 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                    Class: plasmid ends
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/Clome_11b="Mouse 10kb plasmid UUGC1M 11brary"
/note="Vector: pw82nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
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/strain="C57BL/6J"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Welse,R. Mouse whole genome scaffolding with paired end reads from 10kb
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                      High quality sequence stop: 28.
Location/Qualifiers
                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0327 row: F column: 02
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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; Pred. No. 1.2e.
0; Mismatches
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114]gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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RESULT 1103 AZ653365/c Best Matches Query Match Local 4012 AAAATGAGAAAAAAGAGAGAAAAACAAAA 4039 21; Similarity 75.0 21; Conservative AAAAAAAAAAAAAAAAAAAAAAAAAAA 28 0.2%; <u>,</u> Score 16.8; DB 1; Pred. No. 1.2e+03; 0; Mismatches 7; Length 28; Indels **,** ٥,

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DEFINITION

GSS 14-DEC-2000

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SOURCE ORGANISM REFERENCE FEATURES COMMENT VERSION **EYWORDS** ACCESSION JOURNAL TITLE AUTHORS source Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 28)

1 (bases 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Contact: Robert B. Weiss University of Utah Genome Center University of Utah AZ653365 28 bp DNA linear GSS 14-DEC-20 1M0527E02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0527E02 F, genomic survey sequence. Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Insert Length: 10000 Std Error:
Plate: 0527 row: E column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT Tel: 801 585 5606 Fax: 801 585 7177 Unpublished (2000) Mus musculus AZ653365.1 GI:11790511 GSS. plasmid inserts Mouse whole genome scaffolding with paired end reads from 10kb Mus musculus (house mouse) ass: plasmid ends gh quality sequence stop: 28. 308, USA Biomedical Polymers Research Bldg., Location/Qualifiers 0.00 20 S. 2030 E., SLC,

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JOURNAL COMMENT
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AZ785035/c
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AUTHORS
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Best Local Similarity
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: J column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                          quality sequence stop: 28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA
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/strain="C57BL/6J"
                                                                                 Location/Qualifiers
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'clone="UUGC1M0527E02"
'mol_type="genomic DNA"
                         organism="Mus musculus"
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Pred. No. 1.2e+03;
0; Mismatches 7;
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KEYWORDS VERSION

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ACCESSION

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AZ824519/c
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Best Local
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                                            source
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                                                                                                                                    Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0099 row: I column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 28)
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                                                                                                                                                                                                                                                                                                                                   University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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                                                                    quality sequence stop: 28.
Location/Qualifiers
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWPA2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC2M0028J01"
/organism="Mus musculus"
/mol_type="genomic DNA"
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Pred. No. 1.
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                                                                                                                                                                                  Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
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2M0115D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0115D04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                  lass: plasmid ends
igh quality sequence stop: 28.
Location/Qualifiers
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                            /organism="Mus musculus"
/mol_type="qenomic מאר"
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/clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Durified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0099I09"
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75.0%;
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Matches

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SOURCE **KEYWORDS** VERSION

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                  High quality sequence stop: 28.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ866569 28 bp DNA linear GSS 21-FEB-200 2M0177B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0177B08 F, genomic survey sequence.
                                                                                                                                                                                                               Plate: 0177 row: B column: 08 Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0177 row: B column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 28)
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                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 1.2e+03;
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Constructed at the Institute for Genomic Research (TIGR),

Constructed At the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                            Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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GSS.
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T. brucei sheared genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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/note="Vector: PW923ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/db_xref="taxon:5691"
/clone="291a01"
                                                                                   /organism="Trypanosoma brucei"
/mol_type="genomic איאית"
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/strain="TREU927"
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VERSION KEYWORDS

ACCESSION

DEFINITION TA291A01Q RESULT 1108

SOURCE

ORGANISM

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AUTHORS

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                                                                                                                                                            ACCESSION
                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                         TA29A09P/c
                                                                                                                                                                                                                                                                RESULT 1110
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TA379D11P/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li Submitted (10-120-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 15A, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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                                                                                                                                       genomic survey of AL453073 AL453073.1 GI:
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T. brucei sheared genomic
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T. brucei sheared genomic
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
                                                                               Trypanosoma brucei
                                                                                                                    GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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                                                                                                Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                     Trypanosoma.
                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                (bases 1 to 28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="379d11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Trypanosoma brucei"
                                                                                                                                         GI:11854584
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 Mismatches

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Pred. No. 1.
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CF279536/c
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Best Local Similarity
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 bp mRNA linear EST 14-AUG-20
14ETL--05-N22.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-N22, mRNA sequence.
CF279536
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 29)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                               Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF279536.1 GI:33656922
EST.
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4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
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                /mol type="mRNA"
/cultivar="Wackdong"
/db xref="taxon:4530"
/clone="14ETL--05-N22"
/clone="14ETL--05-N22"
/tlssue_type="leaf"
/dev_stage="14 days after germination"
/lab host="E.coll DH10B"
/clone_lib="Rice etiolated leaf plasmid c
                                                                                                                                                                                                                                                    bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
/cione_lib="Rice etiolated leaf
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/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                         organism="Oryza sativa"
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/clone="29a09"
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Pred. No. 1.2e+03;
0; Mismatches 7
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                   plasmid
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                     cDNA library
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Matches 21
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Best Local
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                                    CF312601.1 GI:33684362
EST.
                                                                                        CF312601 29 bp mRNA linear EST 15-AUG-2003 ABF--08-G22.gl ABF3-overexpressing transgenic rice plasmid cDNA Library (ABF) Oryza sativa cDNA clone ABF--08-G22, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeenggi, Kyeeng MyongJi, Korea Tel: 82 31 330 6193

Tel: 82 31 330 6193

Tex: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 АЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 2
Oryza sativa
                Oryza sativa
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Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capps
with oligoribonucleotides and then used as templates fr-pCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--04-C02"
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with oligoribonucleotides and then used as templat
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                          Score 16.8; I
Pred. No. 1.3e
0; Mismatches
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bhnahm@bio.myongji.ac.kr
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(7LEAF) Oryza
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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COMMENT
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ORGANISM
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AZ389566
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                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 29)
1 (Dases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ389566 29 bp DNA linear GSS 02-OCT-20 1M0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150D21 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,B.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                     Plate: 0150 row: D column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 21
                                                                                                                                                                             University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
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AZ389566.1 GI:10503274
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Ehrhartoideae; Oryzeae; Oryza.
Class: plasmid ends
                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Location/Qualifiers
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Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="14 days after germination"
/lab_nost="s.coli DH108"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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cultivar="Nackdong"
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clone="ABF--08-G22"
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Pred. No. 1.3e+03;
n: Mismatches 7;
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                                                                                                                                                                             Bldg.,
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AZ414283/c
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Best Local Similarity
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.000

Plate: 0188 row: G column: 12

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                  University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1M0188G12R Mouse 10kb plasmid clone UUGC1M0188G12 R, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High
                                                                                                                                                                                                                                                                                                     84112, USA
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWH042 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant,
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42ny; Purified genomic DNA from Note="Vector: PWD42ny; Purified genomic DNA from Note="Note: PWD42ny; Purified genomic DNA from Note: PWD42ny; PWD
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/strain="C57BL/6J"
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Pred. No. 1.3e+03;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
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1 (bases 1 to 29)
1 (bases 1 to 29)
1 (bases 1, to 2
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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/strain="C57BL/6J"
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Pred. No. 1.3e+03;
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                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Bror:
Plate: 0281 row: G column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 29)
High quality sequence stop: 29.
Location/Qualifiers
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Unpublished (2000)
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Fax: 801 585 7177
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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75.0%;
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Pred. No. 1.3e+03;
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                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315N21 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                             High quality sequence stop: 29.
                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                              USA
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/clone="UUGC1M0281G24"
organism="Mus musculus"/
                                              Location/Qualifiers
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strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beacorn, T., Duval, B., Hamil, C.,
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1.3e+03;
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Best Local Similarity
                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedereen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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1M0540K20F Mouse 10kb plasmid UUGCIM library Mus musculus
clone UUGCIM0540K20 F, genomic survey sequence.
                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0540 row: K column: 20
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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                                                                       quality sequence stop: 29.
Location/Qualifiers
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/Clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
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/clone="UUGC1M0315N21"
mol_type="genomic DNA"
                       organism="Mus musculus"
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Pred. No. 1.
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AZ784208
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Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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Mouse whole genome scaffolding with paired end reads from 10kb
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Seq primer: CACACAGGAAACAGCTATGACC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
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                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                  organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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75.0%;
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Best Local Similarity
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                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0068 row: I column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Federsen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 29)
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                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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igh quality sequence stop: 29.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                    USA
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson
/organism="Mus musculus'
/mol_type="genomic DNA"
/strain="C57BL/6J"
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RESULT 1122
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Best Local
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                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
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Unpublished (2000)
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                                                                                                                                                                                       High quality sequence stop: 29.
                                                                                                                                                                                                                   Class: plasmid ends
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114 [gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UUGC2M0068I02"
                      /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                             Cocation/Qualifiers
clone="UUGC2M0078J15"
                                                                                                      organism="Mus musculus"
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Pred. No. 1.3e+03;
0; Mismatches 7;
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1.3e+03;
7;
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SOURCE ORGANISM

KEYWORDS

VERSION ACCESSION DEFINITION

REFERENCE

AUTHORS

JOURNAL TITLE

FEATURES

sex="Male"

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REFERENCE
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KEYWORDS
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AZ868731
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Best Local Similarity
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                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                       Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0180 row: L column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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NSA
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                                                                                                                                                             quality sequence stop: 29.
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                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180L02"
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                                                                                                                                    ocation/Qualifiers
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Pred. No. 1.3e+03;
0; Mismatches 7;
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RESULT 1124
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                                                                                                                                                                                                                                                                                                           to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                            Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucel/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing Submitted (10-DEC-2000) Trypanosoma brucei genome Campus, Hinxton, project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
AL491938
AL491938.1 GI:11868238
GSS.
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA334G09Q
T. brucei sheared genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nh1@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                          /mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                         organism="Trypanosoma brucei"
                                                                                                                                                                                        Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
clone="334g09"
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Pred. No. 1.3e+03;
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A clone
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REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

FEATURES

Query Match

0.2%; Score 16.8;

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Length 29;

Query Match Best Local Similarity

0.2%;

Score 16.8; DB 1; Pred. No. 1.4e+03;

Length 30

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REFERENCE
AUTHORS
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AZ458127/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0261 row: I column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ458127 30 bp DNA linear GSS 04-OCT-20
1M0261124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261124 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 30.
Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male"
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RESULT 1127
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Best Local Similarity
Matches 21; Conserv
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CF280699 30 bp mRNA linear EST 14-AUG-20 14ETL--07-H15.bl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--07-H15, mRNA sequence. CF280699 GF280699.1 GI:33658085
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Rattus norvegicus
Bukaryota; Metazoa; Chordata;
Bukaryota; Mutheria; Rodentia;
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DRACRC02 Rat DRG Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031,
Tel: 86-21-64748700-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 30)
Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Xiao,H.S., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axocomy model of neuropathic pain
in the rat peripheral axocomy model of neuropathic pain
proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG666435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T3 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: T3
BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
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l: xu.zhang@ion.ac.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                               /tissue_type="dorsal root ganglion"
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                                                                                                                                                                                                                                                                                                                                           clone_lib="Rat DRG Library"
                                                                                                                                                                                                                                                            0.2%; Score 16.8; DB 1; Length 30; 75.0%; Pred. No. 1.4e+03; tive 0; Mismatches 7; Indels
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Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 30)
1 (bases 1 to 30)
1 (Song, S. I., Kim, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y.C., Song, S. I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 30)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin, Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                 Genomics and Genetics Institute, (
of Bioscience and Bioinformatics,
                                                                                                                                                                                                                         Contact: Nahm B.H.
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                                                                                                                     gin, Kyeonggi, Ko
: 82 31 330 6193
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                                                                              bhnahm@ggbio.com, bhna
Location/Qualifiers
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  organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="14ETL--07-H15"
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                                                                                                                                                                 Korea
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; Pred. No. 1.4e
0; Mismatches
                                                                                                     bhnahm@bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 bp
                                                                                                                                                                               GreenGene Biotech Inc.; Division, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4e+03;
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CDNA library (14ROOT) Oryza
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CF299555/c
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CF312417

30 bp mRNA linear EST 15-AUG-2003
ABF--08-C19.bl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-C19, mRNA sequence.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Ouyza sativa
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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EST.
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                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
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/mol'type="mRNA"
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/cullivar="Nackdong"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-70PO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bhnahm@ggbio.com, bhna
Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Pred. No. 1.4e+03;
0; Mismatches 7;
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Pred. No. 1.4e+03;
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(7LEAF) Oryza
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidaae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
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CF312417.1
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/lab_host="5.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid /clone_lib="ABF3-overexpressing transgenic rice plasmid /cDNA lībrary (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4530"
/clone="ABF--08-C19"
/tissue_type="leaf"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 1.4e+03;
0; Mismatches 7;
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 30)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NACL--02-H17.gl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-H17, mRNA sequence.
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ААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 28
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                              bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                  /cullivar="Nackdong"
/db xref="taxon:4530"
/clome="NACL--02-H17"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clome_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
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/clone="HD--13-M02"
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|mol_type="mRNA"
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; Pred. No. 1.4e
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Pred. No. 1.4e+03;
0; Mismatches 7;
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Best Local :
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
Unpublished (2000)
                                                                                                                                                                    Mus musculus (house mouse)
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--06-K13"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                              AZ357603 30 bp DNA linear GSS 0.1 100099H17F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0099H17 F, genomic survey sequence.
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JMT--06-K13.gl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-K13, mRNA sequence.
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Pred. No. 1.4e+03;
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RESULT 1135
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AUTHORS
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                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi. 1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                            AZ443322
30 bp DNA linear GSS 0-
1M0237L20R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0237L20 R, genomic survey sequence.
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                              Mus musculus
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Insert Length: 10000 Std Error:
Plate: 0099 row: H column: 17
                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                     AZ443322.1 GI:10591190
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
                                                 plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD2 (gil 4732114 | gb| AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0099H17"
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75.0%;
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Pred. No. 1.
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                       JOURNAL
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                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                               AZ455741 30 bp DNA linear GSS 04-OCT-200 IM0258016F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0258D16 F, genomic survey sequence.
AZ455741
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 30)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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Seq primer: CACACAGGAAACAGCTATGACC
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Insert Length: 10000 Std Error: 0.00
Plate: 0237 row: L column: 20
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
0.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMay2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC1M0237L20"
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                 Euteleostomi;
; Murinae; Mus
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AZ481739/c
                                                                                                                               TITLE
                                                                                                                                                                                                                                   AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ481739 30 bp DNA linear GSS 04-OCT-20: 1M0306N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0306N12 F, genomic survey sequence.
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Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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High quality sequence stop: 30.
Location/Qualifiers
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                Mus musculus
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Insert Length: 10000 Std Err
Plate: 0258 row: D column: 1
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                                                                                                                            Mouse whole genome
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                  AZ481739.1 GI:10642804
                                                                                                                                                                                                                                                                                                                                                           fus musculus (house mouse)
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWM92 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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strain="C57BL/6J"
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                                                                                                                         scaffolding
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Rodentia;
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                                                                                                                         with paired end reads from 10kb
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AZ582114/c
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Best Local Similarity 75.0
                                                                                                           JOURNAL
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Mus musculus (house mouse)

Mus musculus
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: N column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                  1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                               plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 30.
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                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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pred. No. 1.4e+03;
0; Mismatches 7;
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Other ESTS: 2821429.5prime
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
Consortium (LLNL) DNA Sequencing by: Berkeley mGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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AW249485
AW249485.1 GI:6592478
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31 bp mRNA linear EST 07-JAN-2000 2821429.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821429 3',
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fomo sapiens (human)
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0374J17"
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                                              BX569502 31 bp mRNA linear EST 14 EX569502 Glossina morsitans morsitans adult infected gut G morsitans morsitans clone Tse9a03_plc, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: LLCM6 row: M column: 14
High quality sequence stop: 20.
Location/Qualifiers
BX569502.1 GI:33437420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="small cell carcinoma"
/cell line="MGC3"
/lab_host="DHJOB (phage-resistant)"
/lab_host="DHJOB (phage-resistant)"
/clone_lib="NIH MGC_7"
/clone="Torgan: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
/corned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG (G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Stratagene)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                         Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans
Glossina morsitans morsitans
Glossina morsitans morsitans
Elasaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 31)
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at
                                                                                                                                                                                                                                                                                    Genome Biol. 4 (10), R63 (2003) 22881942
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                                                                                                                                                                                                                                    Contact: Hall N
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TITLE
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AUTHORS
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                             4012 AAAATGAGAAAAAAGAGAGAAAACAAAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 31)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., I
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF278807.1 GI:33656193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                            bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cDNA all plc reads
                                                                                                                            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                          /clone="14ETL--04-N15"
/tissue_type="leaf"
/tissue_type="1eaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="Tse9a03 plc"
/tissue type="adult infected gut"
/tione_lib="Glossina morsitans mo
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                             db_xref="taxon:4530"
                                                                              0.2%;
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                                                             Score 16.8; I
Pred. No. 1.4e
0; Mismatches
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lleaf pla
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plasmid cDNA library (14ETL)
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                                                               7;
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                                                                                            Length 31;
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ORGANISM
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CF300345/c
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AZ333315/c
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                                                                   Julii, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10th plasmid inserts
                                                                                                                                                                                                                                                                                                             AZ333315
AZ333315.1
GSS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
--1-- Mahhmoud M. Meenen E., Pedersen,T.,
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IM0062A21F Mouse 10kb plasmid clone UUGC1M0062A21 F, genomic
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1 (bases 1 to 31)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Contact: Robert B. University of Utah University of Utah
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Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
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82 31 321 6355
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7lEAF--04-L08"
/clone="7lEAF-04-L08"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
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Pred. No. 1.4e+03
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
                       Center
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UUGC1M library Mus musculus
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(7LEAF) Oryza
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse, whole genome scaffolding with paired end reads from 10kb
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1M0129D08R Mouse 10kb plasmid clone UUGC1M0129D08 R, genomic
                                                                                     Contact: Robert B.
                                                                                                          Unpublished (2000)
                                                                                                                                        plasmid inserts
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Fax: 801 585 7177
Email: dduurn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0062 row: A column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARARARARARARARARARARARARARA
                                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
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Location/Qualifiers
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/clone_lib="Mouse_lokb plasmid_UUGC1M_library"
/note="Vector: PMD42nv; Purified_genomic_DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWH92 (gil 4732114 [gb] AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
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/clone="UUGC1M0062A21"
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/strain="C57BL/6J"
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
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AZ510092
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KEYWORDS
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                                                                                  plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 bp DNA linear GSS 05-OCT-200 1M0354P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0354P14 F, genomic survey sequence.
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Insert Length: 10000 Std Error: 0
Plate: 0129 row: D column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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Location/Qualifiers
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC1M0129D08"
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                                                                                        Weiss
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AZ623538/c
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                                           University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res
                                                                                                                                                    Diasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1M0461G21F Mouse 10kb plasmid clone UUGC1M0461G21 F, genomic
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Insert Length: 10000 Std Erry
Plate: 0354 row: P column: 1
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                                                                                                                            Contact: Robert B.
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Location/Qualifiers
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801 585 5606
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pNN942 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354P14"
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Pred. No. 1.4e+03;
"Amatches 7; Indels 0;
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UUGC1M library Mus musculus genomic
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AZ627692
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Best Local Similarity
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Insert Length: 1000 Std Error:
plate: 0461 row: G column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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31 bp DNA linear GSS 13-DEC-200
1M0469C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0469C09 R, genomic survey sequence.
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stekes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                      University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                       plasmid inserts
Unpublished (2000)
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                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PW9270x; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso)
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/clone="UUGC1M0461G21"
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/strain="C57BL/6J"
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AZ778697
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                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse, whole genome scaffolding with paired end reads from 10kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 bp DNA linear GSS 100014002F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC2M0014002 F, genomic survey secretion AZ778697
                            Tel: 801 585 5606
Fax: 801 585 7177
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Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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                                                                                 USA
ddunn@genetics.utah.edu
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 1.
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Dunn, D., Aoyagi, A.; Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                              Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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Plate: 0014 row: O
Smail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 (gi|4732114|gb|AF199072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Noese whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0102 row: C column: 19
                                                                                                                                                                                Contact: Robert B. Weiss University of Utah Genome University of Utah
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 31)
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31 bp DNA linear GSS 20-FEB-20 2M0102C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102C19 F, genomic survey sequence.
                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                  USA
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strain="C57BL/6J"
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ486763 31 bp DNA linear GSS 0: 1M0315A11F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0315A11 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Sd Error:
Plate: 0315 row: A column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                      Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 31)
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                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                          plasmid inserts
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                                                                                                                                                                     308,
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                                                                                                                                                 USA
                                                                                                                                                                     Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" (clone_lib="Mouse 10kb plasmid UUGCIM library" (note="Vector: pwp82ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
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/strain="C57BL/6J"
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Pred. No. 1.4e+03;
0; Mismatches 7
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                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html plate: LLCM0028 row: G column: 13 Seq primer: -21M13 forward primer (ABI). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW327277 32 bp mRNA linear EST 28-JAN-2000 dq01d07.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
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High quality sequence stop: 31.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW327277.1 GI:6797772
                                                                                                                                                                                                                                            cDNA Library Preparation: Edge BioSystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: NIH Intramural Sequencing Center (NISC)
clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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/clone="UUGC1M0315A11"
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/strain="C57BL/6J"
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CF291773/c
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CF299386/c
                                                              DEFINITION
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Best Local Similarity 75.0%;
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Sativa cDNA clone 7DEAF-
CFZ99386
CFZ99386.1 GI:33671147
EST.
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                                            CF299386 32 bp mRNA linear 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--03-G07, mRNA sequence.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 bp mRNA linear EST 14-AUG-:
14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-F12, mRNA sequence.
CF291773
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF291773.1 GI:33660806
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                                                                                                                                                                                                                                                                     /tissue_type="T cell leukemia"
/cell līne="MGC2"
/clone_lib="NIH_MGC_2"
/note="Organ: Blood; Vector: pOTB7a; Library prepared
Edge BioSystems."
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:4530"
clone="14ROOT--02-F12"
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75.0%;
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Pred. No. 1.5e+03;
0; Mismatches 7
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(7LEAF) Oryza
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                of Bioscience and Bioinformatics,
Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Similarity 75.0%;
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82 31 321 6355
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Location/Qualifiers
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/tissue_type="leaf"
/dev_stage="7 days after germination"
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/mol_type="mRNA"
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/cultivar="Nackdong"
/clone="ABF--03-F14"
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                                                                                                                                                  bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                       MyongJi University
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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ABF--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--03-I03, mRNA sequence.
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CF309345.1 GI:33681106
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF--03-I03"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
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/note="Vector: pCR4-TOP0; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped MRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                             /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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0; Mismatches
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Pred. No. 1.5e+03
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                             HD--12-C15.g1 OsHDAC1-overexpressing library (HD) Oryza sativa cDNA clone CF321046
                                                                                       Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 32)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
                                                                     Contact: Nahm B.H.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site_1: ECORI; Callus was treated with ABA(20um) for ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
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/clone="HD--01-P05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; Di
Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              32 bp
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                                                                                                                                                                                                                                                                                                                                                                 RNA linear EST 15-AUG-2003 transgenic rice plasmid cDNA HD--12-C15, mRNA sequence.
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TITLE
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CF328471/c
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  Query Match
Best Local S
Matches 21
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Best Local S
Matches 21
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF328471 32 bp mRNA linear EST NACL--03-G09.bl Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-G09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sativa cDNA clone
CF328471
n 0.2%;
Similarity 75.0%;
21; Conservative
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Fax: 82 31 321 6355
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                                                                                                    /organism="Oryza sativa"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
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/culTivar="Nackdong"
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/clone="NACL--03-G09"
/clone="NACL--03-G09"
/tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com, bhn
Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="05HDAC1-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--12-C15"
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/mol_type="mRNA"
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Score 16.8; DB 1;
Pred. No. 1.5e+03;
0; Mismatches 7
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Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          bhnahm@bio.myongji.ac.kr
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CF331270/c
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AZ459536/c
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Best Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                            AZ459536 32 bp DNA linear GSS 04 1M0264M16F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0264M16 F, genomic survey sequence.
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NACL--07-F08.bl Rice callus plasmid cDNA library (NACL) Oryza
Sativa cDNA clone NACL--07-F08, mRNA sequence.
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AZ459536.1 GI:10617577
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%;
Similarity 75.0%;
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Location/Qualifiers
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/tissue_trype="callus"
/tissue_trype="callus"
/dev_stage="proliferrated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Oryza sativa"
(mol_type="mRNA"
(cultivar="Nackdong"
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Pred. No. 1.5e+03;
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AZ470832
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Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederbausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Nouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                        AZ470832.1 GI:10628957
GSS.
                                                                                                                                                                                                                                                                                                                                                    AZ470832 32 bp DNA linear GSS 04-OCT-20
1M0285F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0264 row: M column: 16
Seq primer: CGTTGTARAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                clone UUGC1M0285F14 F, genomic survey sequence.
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USA
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42ny, Purified genomic DNA from !
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/strain="C57BL/6J"
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Genome Center
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Pred. No. 1.5e+03;
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AZ611890/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                     32 bp DNA linear GSS 13-DEC-20 IM0438E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0438E02 R, genomic survey secuence AZ611890
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Tel: 801 585 5606
Fax: 801 585 7177
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                     Mus musculus
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High quality sequence stop: 32.
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Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: F column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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/strain="C57BL/6J"
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Pred. No. 1.5e+03;
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Best Local Similarity
                                                                                                                                                                               AUTHORS
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                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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32 bp DNA linear GSS 16 2M0012020R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC2M0012020 R, genomic survey sequence.
                          plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Error: C
Plate: 0438 row: E column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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Fax: 801 585 7177
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4012 AAAATGAGAAAAAAAGAGAGAAAAAA 4039
                   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidormes; Cyprinidae; Danio.
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Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: 0 column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Class: plasmid ends
Location/Qualifiers
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Fax: 801 585 7177
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                Humphray, S.J., Huckle, E. and Hunt, S.E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                 Danio rerio
                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                          AL986044.1 GI:25187956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi |4732114 |gb |AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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DEFINITION

BU431798 33 bp mRNA linear EST 09-bt 601655890R1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3855694

EST 09-SEP-2002

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RESULT 1166
CF334899/c
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                                                                                                                               4012 AAAATGAGAAAAAAGAGAGAAAAACAAAA 4039
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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library (JMT) Oryza sativa cDNA clone JMT--04-F19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF334899.1
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxxon:4530"
/clone="JWT--04-F19"
                                                                                                                                                                                                                                                           /dev_stage="14 days after germination"
/lab_host="E.Coli DH10B"
/clome lbb="AtLMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TopO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                         methyltransferase overexpression line."
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-85L21"
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Pred. No. 1.5e+03
0; Mismatches
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plasmid cDNA
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CF291613/c
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
            Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                             Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                            Bativa cDNA clone 14ROO
CF291613
CF291613.1 GI:33660646
                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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High quality sequence stop: 31.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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BU431798
BU431798.1 GI:22770280
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 33)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma"
/lab_host="DH10B (phage resistant)"
/clone_libe="NIH_MGC_66"
/clone_tibe="NIH_MGC_66"
/note="Organ: Ovary; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
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_xref="taxon:9606"
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14ROOT--02-B21, mRNA sequence.
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; Pred. No. 1.5e
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Best Local Similarity
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
Oryza sativa
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33 bp mRNA linear EST 15-AUG-2003
ABF--06-F23.gl ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--06-F23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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    Conservative
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                                                                                                  /organism="Oryza sativa"
/mol type="mRNA"
/mol type="mRNA"
/cultivat="Nackdong"
/cultivat="Nackdong"
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/clone="ABF--06-F23"
/tissue_type="leaf"
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/dev_stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/clone="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for Zhrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                    bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-B21"
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75.0%;
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Score 16.8; DI
Pred. No. 1.5e.
O; Mismatches
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Pred. No. 1.5e+03;
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RESULT 1171
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CF326967
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Informatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
                                                                                                     1 (bases 1 to 33)

Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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NACL--03-C14.g1 Rice callus plasmid cDNA library sativa cDNA clone NACL--03-C14, mRNA sequence.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                          Oryza sativa
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                                                                                                                                                                                                                                                                                              Oryza sativa
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82 31 330 6193
82 31 321 6355
1: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="taxon:4530"
/clone="NACL--01-E04"
/tissue_type="callus"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E_coli_DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 1.5e+03;
0; Mismatches 7;
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                                                              Biotech Inc.; Division
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(CL) Oryza
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                 Query Match
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatroideae; Oryzeae; Oryza.
 l Similarity
21; Conserv
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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                                                                                                                                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
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                                                                                                                                                                                                                                         /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="texcon:4530"
/clone="JMT--06-019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4530"
/clone="NACL-03-C14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="B.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                      /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtLMT-overexpressing transgenic rice plasmid cDNA lībrary (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoniate Carboxyl methyltransferase overexpression line."
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/mol_type="mRNA"
/cultivar="Nackdong"
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75.0%;
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Score 16.8; Di
Pred. No. 1.5e
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Pred. No. 1.5e+03
                                                                                                                                                                                                                                                                                                                                                                         bhnahm@bio.myongji.ac.kr
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                      1.5e+03
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                                        DB 1;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, N., Rockes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                           AZ486795 33 bp DNA linear GSS 05-OCT-20 1M0315P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315P22 F, genomic survey sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 33)
                                                                                                                                                                                                   Mus musculus
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                    Mus musculus (house mouse)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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/lab_host="E_coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA llbrary (JMT)"
/note="Vector: pCR4-TOP0; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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/clone="JMT--07-G18"
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/cultivar="Nackdong"
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Unpublished (2000)
Contact: Robert B. W
University of Utah C
University of Utah
Rm. 308, Biomedical
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 33)
                                                                                                                                                                                                                                                                                                1M0474B02F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0474B02 F, genomic survey sequence.
AZ627839
                                                                                                                                                                                                    Mus musculus
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0315 row: P column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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Insert Length: 1000 Std Error: 0.00
Plate: 0474 row: B column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Clabs: plasmid ends
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 41A4. 41A4 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                           Submitted (14-NOV-2002) The Sanger Institute, V Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 34)
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                             Humphray, S.J., Huckle, E. and Hunt, S.E. Direct Submission
                                                                                                                                                                                                                                                                            Danio rerio
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/strain="C57BL/6J"
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                                                                             Wellcome Trust Genome . E-mail contact:
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         7LEAF--04-H15.bl Rice leaf plasmid cDNA linear 7LEAF--04-H15.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--04-H15, mRNA sequence. CF300172 CF300172.1 GI:33671933 EST.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 23)
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda, Makeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
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AU267170 VS Dictyostelium
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Location/Qualifiers
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-298-53-4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Biological Sciences
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/clone="DKEY-41A4"
/tissue +v== "-
                                                                                                                                                                                                                                                                                                      /dev_stage="vegetative"
/clone_lib="VS"
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                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:44689"
/clone="VSH269"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Dictyostelium
/mol_type="mRNA"
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/mol_type="genomic DNA"
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Pred. No. 9.4e+02;
0; Mismatches 4;
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Pred. No. 1.6e+03;
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(7LEAF) Oryza
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RESULT 1179
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.,
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 23)
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J.,
Kim,J.K., Kim,Y.-K. and Nahm,B.F
Song,S.I., Kim,J.K., Kim,Y.-K. and Rice ES'
                                                                                                                                                                                         Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                 Large-scale Sequencing Analysis 
Unpublished (2003)
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EST.
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7LEAF--07-F21.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
81 STATURA CDNA Clone 7LEAF--07-F21, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                            bhnahm@ggbio.com, bhna
Location/Qualifiers
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/tissue_type="leaf"
/dev grage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with_oligoribonucleotides and then used as templates for
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/clone="7LEAF--07-F21"
/tissue_type="leaf"
                                                              /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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Pred. No. 9.4e+02;
0; Mismatches 4;
                                                                                                                                                                   bhnahm@bio.myongji.ac.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rockes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ374746 23 bp DNA linear GSS 02-OCT-20 1M0127D15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127D15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0127 row: D column: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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llarity 82.6%;
Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                           /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC1M0127D15"
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                                                                                                                                                                                                                                                                                                                                                                                         sex="Male"
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Pred. No. 9.4e
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and

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JOURNAL COMMENT
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AZ469557
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0283 row: A column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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1M0283A09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0283A09 F, genomic survey sequence
AZ469557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated in the blust derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                              clone="UUGC1M0283A09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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Pred. No. 9.4e+02;
complementary to the insert adaptors and
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AV740046
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            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zhu Chen
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                         HNC5-1-D5.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road. Zhangjiang Hi- Took Dark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 25)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AV740046.1 GI:10857627
                                                             BG925523.1
                                                                                                                           BG925523
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mbshi@ms.stn.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFAWF04"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript; Site 1: EcoRI;
cloned randomly with the EcoRI digestion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                             GI:14320046
                                                                                                          HNC (Human Normal
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                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                Score 16.6; DB 1;
Pred. No. 1.1e+03;
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Pred. No. 9.4e+02;
0; Mismatches 4;
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l Cartilage) Homo
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                                                                                                                                                                                                                                                                                              Length 25;
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                                                                                                          sapiens cDNA,
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF297950 25 bp mRNA linear EST 15-AUG-207LEAF--01-C05.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
                                                                                                                                                                                                                                                                                        Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF297950.1 GI:33669711
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Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 Swedeland
Tel: 610-270-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sativa cDNA clone 7LEAF--01-C05, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Kyeonggi,
/organism="Oryza sativa"
/mol type="mRNA"
/culfivar="Wackdong"
/db_xref="Wackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-CO5"
/tissue_type="leaf"
/dev_stage="7 days after germination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Directional"
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/lab_host="E.coli pH10 B"
/clone_llb="HNC (Human Normal Cartilage)"
/note="Vector: psporT I; Site_1: SalI; Si
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/db_xref="taxon:9606"
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Pred. No. 1.1e
O; Mismatches
                                                                                                                                                                                                                                                                                                                         bhnahm@bio.myongji.ac.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0072 row: J column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ340193.1 GI:10415397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%;
Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTTTTTTTTTGGATAAGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 25)
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNDA2 (gi|4732114|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="UUGC1M0072J03"
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Pred. No. 1.1e+03;
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."

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REFERENCE
AUTHORS
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KEYWORDS
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AZ510562/c
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GGAAGGGAAGGAAGGAAGGGC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: F column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ510562 25 bp DNA linear GSS 05-OCT-200100355F11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0355F11 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
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19; Conservative
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801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 bx range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"

(mol_type="genomic DNA"

(strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC1M0355F11"
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AL048684
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AUTHORS
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KEYWORDS
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SOURCE
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                    4017 GAGAAAAAAGAGAGAAAACAAAA 4039
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 30)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 30)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
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DKFZp566C043 rl 566 (synonym:
DKFZp566C043, mRNA sequence.
AL048684
                                                                                                                                                                                                                                     AL048732

DKFZp5661053_r1 566 (synonym: hfkd2) Homo
DKFZp5661053, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MIPS
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AL048684.1 GI:4727755
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              Contact:
                                                                                                                                                                                                         AL048732.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
                                                                                                                                                                           lomo sapiens (human)
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ilarity 82.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="x1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKFZp566C043"
/tissue_type="kidney"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Pred. No. 1.1e+03;
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: hfkd2) Homo
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sapiens
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R59306/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 32)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RES9306 32 bp mRNA linear EST 24-N yh16c10.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:37903 3' similar to gb:M29064 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R59306.1 GI:830001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp5661053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_hoste_xxl-zblue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: Sall"
                                                                                                                                                                                                                                   /db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Matches 22
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                                  ORGANISM
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                                                                                                    sequence.
BM658677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF328492 34 bp mRNA linear BST NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-G22, mRNA sequence. CF328492
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                     LZV602768363.R1 CSEQFXL37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
Oryza sativa
                                  Sus scrofa
                                                  Sue ecrofa
                                                                                    BM658677.1
                                                                                                                                                       BM658677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF328492.1 GI:33805230
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
/ith oligoribonuclectides and then used as templates for
\u03b3-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="NACL--03-G22"
/fissue_type="callus"
/dev_stage="proliferated callus on 2N6 media
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers,
                                                  (pig)
                                                                                    GI:18958948
                                                                                                                                                                                                                                                                                                                              0.2%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                     pig
                                                                                                                                     1.6e+03;
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                                                                                                                                                                                                                                                                                                                                            Length 34;
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Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for 30 days"
                                                                                                                                                       27-FEB-2002
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CF300456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                    Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF300456 18 bp mRNA linear EST 15-AUG-2003
7LEAF--04-N23.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-N23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: David L. Adelson
Animal Breeding and Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adelson, D.L. and Gill, C.A. Porcine ESTs
                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
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Similarity 94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Animal Science Dept., TAMU-2471, College Station,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9798452616
9798456970
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                                                                                                                                                                                                                                                                                               bhnahm@ggbio.com,
                                                                                                                                /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--04-N23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9823"
/db_xref="taxon:9823"
/clone_lib="CSEQFXL37 pig adrenal"
/note="organ: adrenal gland; Vector: pBluescript SK+;
Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (5'-NNN. ..NNNINBERT)
GCGAATTGGAGCTCCACCGCGGTGGCGGCGCGCGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAC
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was capped
with_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-normalized library, sequenced 3' with M13R primer."
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Pred. No. 6e+02;
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                                                                                                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
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RESULT 1194
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Best Local
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17; Conserv
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1 (bases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                  CF320046
HD--10-M11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDlibrary (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
                                                                          Oryza sativa
                                                                                                Oryza sativa
                                                                                                                                     CF320046.1 GI:33691807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University
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7LEAF--07-N19.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
Bativa CDNA clone 7LEAF--07-N19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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: 82 31 330 6193
: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Naskdong"
/db_xref="taxon:4530"
/clone="7LEAF-07-N19"
/clone="7LEAF-07-N19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/note="Vector: pCR4 TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Pred. No. 6e+02;
0; Mismatches 1;
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Pred. No. 6e+02;
0; Mismatches
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CF329137/c
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Best Local Similarity
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                                                                                                                                                                                                                                                               Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                           Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
/tissue_type="callus"
/dev_stage="proliferated
/lab_host="E.coli_DH10B"
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/mol_type="mRNA"
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                                                               /clone="NACL--04-F15"
                                                                               /cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                      organism="Oryza sativa"
|mol_type="mRNA"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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/clone="HD--10-M11"
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                      media
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RESULT 1197
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ORGANISM
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CF334610
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Best Local Similarity
Matches 17; Conserv
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JOURNAL
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Best Local :
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
AZ360314 19 bp DNA linear GSS 02-OCT-2001M0103603R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103G03 R, genomic survey sequence.
AZ360314
AZ360314.1 GI:10474014
GSS.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene of Bioscience and Bioinformatics, MyongJi U
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="14 days after germination"
|lab_host="E.coli DHIOB"
|clone lib="AtJMT-overexpressing transgenic rice plasmid
|clone library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-P13"
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Pred. No. 6.8e+02;
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Pred. No. 6.8e+02;
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(bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                               19 bp DNA linear GSS 16-FEB-20 1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560L07 R, genomic survey sequence AZ764517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Ingert Length: 10000 Std Error: (
Plate: 0103 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                  TTTTTTTTTCTTTTTT 2
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musculus (house mouse)
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/strain="C57BL/6J"
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                                         GI:12879561
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Resea
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                 CF293087 21 bp mRNA linear EST 14-AUG-30DGS--02-C07.gl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--02-C07, mRNA sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                           Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yonqin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                           In Change 1 to 21)

1 (bages 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Song,S.I., Kim,J.K., Kim,Y.-K. and Rahm,B.H.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                   Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF309614 21 bp mRNA linear EST 15-AUG-2003
ABF--03-N20.gl ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                                                                                                                                                                  Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H
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                                              /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF--03-N20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
/tissue_type="leaf"
/dev_stage="14 days after germination"
                                                                                                                                                                                     Location/Qualifiers
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|mol_type="mRNA"
|cultivar="Nackdong"
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/tissue_type="leaf"
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Pred. No. 8.4e+02;
                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@bio.myongji.ac.kr
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AZ316361/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0034 row: I column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
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1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034I16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 22.
Location/Qualifiers
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                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: pWD42nv; purified_genomic_DNA from M.
musculus_C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse_DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                      sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC1M0034I16"
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Pred. No. 8.4e+02;
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KEYWORDS
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2M0157C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0157C14 R, genomic survey secuence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: C column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pW042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"

(mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="UUGC2M0157C14"
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DEFINITION RESULT 1204 CF292725

CF292725 24 bp mRNA linear EST 14-AUG-30DGS--01-K12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--01-K12, mRNA sequence.

EST 14-AUG-2003

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REFERENCE
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AL587602
                                                    Query Match
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                   4463 CTTTTTTTTTTTTTTT 4481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 23)
s
                                                                                                                                                                                                                                                                                                                                                                                                                    Roslin, Midlothian, EH25 9PS, Tel: +44 (0)131 527 4200 Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Frazer Murray
Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
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AL587602.1 GI:13192636
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                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                     Email: frazer.murray@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP Chicken Brain Library
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                                                                                                                                      Clonetech (*6854-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and selected for ampicillin resistance
                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059F08"
                                                                                                                                                                                                                   /dev_stage="Unknown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                            organism="Gallus gallus"
                                                                                                                                                                                                                                               tissue_type="Brain"
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AI000095/c
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CF292725.1
EST.
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 25)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                  AI000095
AI000095.1 GI:3190649
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI000095 25 bp mRNA linear EST 27-AUC os61a08.sl NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1609814 similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST; contains Li
             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSR1 repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatroideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                        Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="30 days after germination"
/lab_host="E.coli DHIOB"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with olgoribonucleotides and Then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4530"
/clone="30DGS--01-K12"
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Pred. No. 1.1e+03;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 24;
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RESULT 1206
AZ764498/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ACACCAACACCACCACC
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1M0560K04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560K04 R, genomic survey sequence.
                                                                                                        High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0560 row: K column: 04
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                      84112,
                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                               University of Utah
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 1853 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                               308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lab host="DHIOB"
//ab host="DHIOB"
//ab host="MCI_CGAP_Br2"
//clone_lib="NCI_CGAP_Br2"
//clone_lib="NCI_CGAP_Br2"
//note="Vector: p7773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 vector. This library is the normalized version of NCI CGAP_Br1.1 Library was constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg.,
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/tissue_type="breast"
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/db_xref="taxon:9606"
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|mol_type="mRNA"
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 bp DNA linear GSS 16-FBB-20110560L03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560L03 R, genomic survey sequence AZ764502
                                                                                                                                                                                                                                  Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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University of Utah
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                       /organism="Mus musculus"
/mol_type="qenomic מאס"
/db_xref="taxon:10090"
/clone="UUGC1M0560L03"
                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                            ocation/Qualifiers
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2M0087015R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0087015 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffo
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 26.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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'lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                     clone="UUGC2M0087015"
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Pred. No. 1.3e+03;
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TITLE
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ORGANISM
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N89936/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N89936 27 bp mRNA linear EST 02-APR-1996 zb23e12.81 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE: 302926 3' similar to gb:x59066 ATP SYNTHASE ALPHA CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ET primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 8.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRIAL PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/Clone="IMAGE:30236"

/dev stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone lib="Soares fetal lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with

modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1247858"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
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Pred. No. 1.3e+03;
0; Mismatches 6;
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TA257B07P
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                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Librated (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                   4012 AAAATGAGAAAAAAGAGAGAAAACAAA 4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4014 AATGAGAAAAAAGAGAGAAAAACAAAA 4039
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AL483778
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                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucel/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei
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1 (bases 1 to 27)
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AAAAAAAAAAAAAAAAAAAAAA 27
                                                                               0.2%;
ilarity 74.1%;
Conservative
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                                                                                                                                                                 /db_xref="taxon:5691"
/clone="257b07"
                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                organism="Trypanosoma brucei"
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                                                                           Score 16.4; DB 1;
Pred. No. 1.3e+03;
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                                                                                                                       Length 27;
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AUTHORS
LOCUS AZ358038 28 bp DNA linear GSS 02-OCT-20
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                                                                                                                                       RESULT 1212
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2M0079M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0079M06 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: M column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ812708.1 GI:12982221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308,
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for appiciallin vesistance "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="UUGC2M0079M06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4; DB 1;
Pred. No. 1.3e+03;
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                                                      GSS 02-OCT-2000
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RESULT 1213 R16114/c

DEFINITION

R16114

ya51f03.s2 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66461 3' similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE

32 bp

mRNA

linear

EST 13-APR-1995

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
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                                                 4018 AGAAAAAGAGAGAAAACAAAATGTT 4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone UUGC1M0100F05 F, genomic survey sequence. AZ358038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0100 row: F column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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GSS.
AAAAAAAAAAAAAAAAATTTT 28
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pND42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                          purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="UUGC1M0100F05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                             76.9%;
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                                                                                                  0; Mismatches
                                                                                                                             Score 16.4;
Pred. No. 1.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                .4e+03
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                                                                                                                                                         DB 1;
                                                                                                                                                   Length 28;
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VERSION
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AZ316019/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                4011 TAAAATGAGAAAAAAGAGAGAAAACAAAA 4039
                                                                                                                                                                                                                                                                                                              30 TNAANAAANAAAAAAAAAAAAAA 2
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                    AZ316019 21 bp DNA linear GSS 2: 1M0033C05R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0033C05 R, genomic survey sequence.
                                                                                                                  AZ316019
AZ316019.1 GI:10363426
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -21m13
High quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High gality sequence starts: 1
High gality sequence stops: 1
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)
                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R16114
R16114.1 GI:767923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:66461"
                                                                                                                                                                                                                                                                                                                                                                                                       0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 1;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
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                                                             REFERENCE
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AZ345540
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Best Local Similarity
Matches 18; Conserv
                                  AUTHORS
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                                                                                                                                                                                                                                            21 bp DNA linear GSS 29-SEP-201
1M0080P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080P05 F, genomic survey sequence.
A2345540
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                      Mus musculus
                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                 AZ345540.1 GI:10424777
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Unpublished (2000)
Contact: Robert B. Weiss
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Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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High quality sequence stop: 21.
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Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 05
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Pred. No. 9.1e+02;
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                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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AZ346717
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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Insert Length: 10000 Std Erro
Plate: 0080 row: P column: 0
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                                                                                                                                                                                                          GSS.
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AZ346717.1 GI:10425954
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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strain="C57BL/6J"
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Matches 18; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (Dases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                               AZ849030 21 bp DNA linear GSS 2: 2M0150117F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC2M0150117 F, genomic survey sequence.
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Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inverts
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Insert Length: 10000 Std Error:
Plate: 0082 row: O column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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/clone="UUGC1M0082002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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85.7%;
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Pred. No. 9.1e+02;
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                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
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AZ978432
                                                                                                                                                                                                                                                                                                                                            SOURCE
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Best Local Similarity
                  TITLE
                                                                                                                                                                                                                                                                                                       ORGANISM
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                          Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Ielam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ978432 21 bp DNA linear GSS 27-APR-200200254G15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0254G15 R, genomic survey sequence.
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High quality sequence stop: 21.
Location/Qualifiers
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0150 row: I column: 17
           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                               AZ978432.1 GI:13849659
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CGTTGTAAAACGACGGCCAGT
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse_10kb_plasmid_UUGCiM_Ilbrary"
/note="Vector: pM942nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male) was obtained_from_the_Jackson_musculus_C57BL/6J_(male) was obtained_from_the_Jackson_Musculus_C57BL/6J_(mal
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10090"
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TITLE
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COMMENT
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AUTHORS
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VERSION
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CF318882
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ORGANISM
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Best Local Similarity
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0

Plate: 0254 row: G column: 15

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                         I (bases 1 to 22)

Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., L

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                      CF318882 22 bp mRNA linear EST 15-AUG-2003 HD--09-C23.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence. CF318882 CF318882.1 GI:33690643
                                                                                                                                                                                                                                                                                                                             Oryza sativa
Oryza sativa
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                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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(1900)
(Inpublished (2000)
(Contact: Robert B. Weiss
(University of Utah Genome Center
(University of Utah
(University of Utah
(Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 21.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi |4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
muscultus C57BL/6U (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC2M0254G15"
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/strain="C57BL/6J"
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/lab_host="E. coli strain XL10-Gold, T1-resistant,
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                     Lee, T.H., Shin, Y.C.,
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CF328535
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Best Local Similarity
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, (
of Bioscience and Bioinformatics,
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NACL--03-H21.gl Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-H21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhn
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
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82 31 321 6355
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/mol_type="mRNA"
/cultivar="nackdong"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-H21"
/tlssue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/ab host="B.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                        bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--09-C23"
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Pred. No. 9.9e+02;
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                                      4010 СТАРАЛАТБАБАРАЛАРАБАБАБАРАЛАСАРА 4038
29
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E012843-024-019-C03-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA Clone 024-019-C03 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 29 Std Error: 0.00
Plate: 19 row: C column: 03
Seq primer: T7; GTAATACGACTCACTATAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carl-von-Linne Weg 10, 50829 Koeln, Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Leh
and Radelof, U.
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BQ590537.1 GI:26120120
                                                                                                     Similarity
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                                                                                Conservative
                                                                                                                                                                                   Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                       /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Salt, Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Salt 2: Not1;
cDNA library from sugar beet, library provided by KMS
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Sastzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites a)
                                                                                                                                                                RZPD/GABI-Primary database: http://gabi.rzpd.de
                                                                                                                                                                                                                                                  SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="024-019-C03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:161934"
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/mol_type="mRNA"
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                                                                                Pred. No. 1.60
D; Mismatches
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Pred. No. 1.
                                                                                                     Score 16.2; DB 1;
Pred. No. 1.6e+03;
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RESULT 1223
BX551460/c
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VERSION
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TITLE
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Best Local S
Matches 21
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                 JOURNAL
MEDLINE
PUBMED
                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                     32 bp mRNA linear EST 10-OCT-201 BX551460 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tsel18g02_plc, mRNA sequence.
BX551460
BX551460.1 GI:33375626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                         Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases I to 32)
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CA853459

BO8B06.seq CDNA Peking library 12hr SCN3 Glycine max cDNA clone
BO8B06.se, mRNA sequence.

CA853459

CA853459.1 GI:33390252

EST.

Glycine max (soybean)
Glycine max
Glycine max
Glycine max

Chycine max

Spermatophyta; Wagnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Endicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Fabales; Fabales; Fabales; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 32)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from
infected by the soybean cyst nematode
Unpublished (2002)
                                  Genome Biol.
22881942
                                                                                                             Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean Genomics and Improvement Laboratory (SGIL) US Department of Agriculture (USDA), ARS, PSI Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD
Contact: Hall N
                                                                                                morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                  Glossina morsitans morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 504 5750 Fax: 301 504 5728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Alkharouf, N.W.
                   14519198
                                                                             response genes
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="Collar Peking_library_12hr_SCN3"
/clone_Vector: pBluescript_SK-; cDNA_clones_from_mRNA_note="Vector: pbluescript_SK-; cDNA_clones_from_mRNA_extracted_from_roots_of_soybean_cv._Peking_12_hrs_after_infection_by_SCN_race_3. These_are_cloned_in_pBluescript_SK-_phagemid. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3847"
/clone="B08E06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Peking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Glycine max"
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                                                       4 (10),
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Pred. No. 1.7e+03;
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or SCN3 Glycine max cDNA clone
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AZ759642/c
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Matches 21
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Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ759642
33 bp DNA linear GSS 16-FEB-200
1M0552E03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0552E03 R, genomic survey sequence.
                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: B column: 03
                                                                                                                    High quality sequence
                                                                                                                                                         Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                  University of Utah
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are
                                                                                                                                                                                                                                                                                                 Rm. 308,
                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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The Sanger Institute The Wellcome Trust Genome (
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg.,
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.brucei"
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/mol type="mRNA"
/sub species="morsitans"
/db_xref="taxon:37546"
                                                         organism="Mus musculus"
                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="Tse118g02_p1c"
/t18sue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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Pred. No. 1.7e+03;
0; Mismatches 8;
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RESULT 1225
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Best Local Similarity
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33 bp mRNA linear EST 10-OCT-2003
EX558128 Glossina morsitans morsitans adult infected gut Glossina
EX558128 morsitans cDNA clone Tse36g10_p1c, mRNA sequence.
                                                                                                                                                                                                                                                                                School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                               Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hippoboscoidea, Glossinidae, Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hall N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22881942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                               clones with suffix qlc are reverse primer reads starting of the cDNA all plc reads are from 3^\prime end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 |gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                          M.J.Lehane
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/note="Vector: PM942nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
clone="Tse36g10_p1c"
                                                     gus
                                                                          organism="Glossina morsitans morsitans"
| mol_type="mRNA"
                                                                                                                                                                       location/Qualifiers
                       pecies="morsitans"
| xref="taxon:37546"
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Best Local 9
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002) 22362189 12472698
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Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ590166 16 bp mRNA linear EST 06-DEC-2
E012844-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-K18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 16 Std Error: 0.00
Plate: 19 row: K column: 18
Seq primer: T7; GTAATACGACTCACTATAGGGC
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: weisshaa@mpiz-koeln.mpg.de
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                                                                                                Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                         /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Salt; Site 2: Not1;
/note Total from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T.brucei"
                                                                                                                                                                            SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                                                                                                                                                                                                         orientation:
                                                                           RZPD/GABI-Primary database: http://gabi.rzpd.de'
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="storage root"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GABI:189955"
/db_xref="taxon:161934"
/clone="024-019-K18"
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/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Beta vulgaris"
/mol_type="mRNA"
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0.2%; Score 16; DB 1;
100.0%; Pred. No. 5.4e+
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Menze,A., O'Brien,J., Lehrach,H.
                          Length 16
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BQ590207
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BQ592600 16 bp mRNA linear EST 06-S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
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1 (bases 1 to 16)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinf Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien,
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Max-Planck-Institute for Plant Breeding Research
Carl-Von-Linne Weg 10, 50829 Koeln, Germany
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BQ590207.1 GI:26119790
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="storage root"
//lab_host="EMDH10B"
//clone_lib="MMPIZ-ADIS-024-storage root"
/clone_lib="MMPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
CDNA_library_from_sugar_beet, library_provided_by_KMS
CDNA_library_from_sugar_beet, library_provided_by_KMS
Kleinwanzlebener_Saarzucht_AG_Binbeck, Germany, contact:
b.schulz@kws.de; cloning_sites_SalI-NotI, primer_sites_an_
b.schulz@kws.de; cloning_sites_SalI-NotI, primer_sites_an_
                                                                                                                                                                                                                                                                                                                                                      Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/db_xref="taxon:161934"
/clone="024-019-015"
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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100.0%; Pred. No. 5.4e+02;
1ve 0; Mismatches 0;
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                                               EST 06-DEC-2002
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MEDLINE
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Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinf
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S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-028-A01 3-PRIME, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H
                                                                                                                                                                                                                                                                Beta vulgaris
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Insert Length: 16 Std Error: 0.00
Plate: 28 row: F column: 08
Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/clone_lib="MPIZ-ADIS-024-developing root"
/clone_tib="MPIZ-ADIS-024-developing root"
/clone_tib="MPIZ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/cultivar="KWS2320 (double haploid, monogerm breeding
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or other 0;
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RESULT 1230
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LOCUS
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MEDLINE
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Best Local (
                                                                                                                                                                                           TITLE
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                                                                                                                                 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
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1 (bases 1 to 16)
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16 bp mRNA linear EST 06-DEC-2002
E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-H07 5-PRIME, mRNA sequence.
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Insert Length: 16 Std Error: 0.00
Plate: 28 row: A column: 01
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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Max-Planck-Institute for Plant Breeding Research
Max-Planck-Institute for Plant Breeding Research
Core Conference
Pay- 00403715067851
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                           Contact: Weisshaar B
ADIS DNA core facility
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        Max-Planck-Institute
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Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J.,
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/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not!;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not!;
/CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not!, primer sites and
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/lab_host="EMDH108"
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/clone="024-028-A01"
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|mol_type="mRNA"
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ty at MPIZ
for Plant Breeding Research
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JOURNAL COMMENT
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Best Local
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1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF279325.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 bp mRNA linear EST 14-AUG-20 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence. CF279325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
Oryza sativa
                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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/db xref="taxon:4530"
/clone="148TL--05-J09"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:161934"
/clone="024-022-H07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="KWS2320 (double haploid, monogerm breeding
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Pred. No. 5.4e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                    bhnahm@bio.myongji.ac.kr
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CF314377
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Best Local (
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                         CF314377 16 bp mRNA linear EST 15-AUG-2003 HD--02-001.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-001, mRNA sequence.
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library (HD)
CF314377
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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ABF--06-C03.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence. CF311057

CF311057.1 GI:33682818
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Location/Qualifiers
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/cullivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-C03"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stages"14 days after germination"
/lab host="E.coli DH1OB"
/clone lib="ABF3 overexpressing transgenic rice plasmid /clone lib="ABF3 overexpressing transgenic rice plasmid /clone | The Corner | Chap | Corner | Corne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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(14ETL)"
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Pred. No. 5.4e+02;
0; Mismatches 0;
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AUTHORS
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ORGANISM
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VERSION
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KEYWORDS
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Best Local Similarity
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhn.
Location/Qualifiers
                                                                                                                                           1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                         Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, Greendene Biotech I.

of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

(DNA library (HD)"

(note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="callus"
|dev_stage="proliferated callus on 2N6 media for 2 weeks"
|lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4530"
/clone="HD--02-001"
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/cultivar="Nackdong"
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Pred. No.
                     bhnahm@bio.myongji.ac.kr
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o. 5.4e+02;
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                                                            Query Match
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4464 TTTTTTTTTTTTTT 4479
                                          16;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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16; Conserv
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HD--05-D07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.
CF316056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Location/Qualifiers
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/lab_host="E.coli DH10B"
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                                                                                                                                                                                                                                                     tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E_coli DH10B"
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/mol_type="mRNA"
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/clone="HD--04-N10"
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cultivar="Nackdong"
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100.0%; Pred. No. 5.4e+02;
. Mismatches 0;
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                                          Mismatches
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VERSION KEYWORDS

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    TITLE
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                              Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Fax: 82 31 321 6355
1 (bases 1 to 16)

Kim,J.S., Juk,K.M., Cheong,P.J., Kim,M.J., L

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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Location/Qualifiers
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
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Genomics and Genetics Institute, (
Genomics and Benetics Institute, (
of Bioscience and Bioinformatics, 
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.
CF320356
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbbo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Unpublished (2003)
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Location/Qualifiers
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/lab_host="E.coli DH1OB"
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/db_xref="taxon:4530"
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note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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CF327722
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 ORGANISM
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
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JOURNAL
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Best Local Similarity
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                                                                                         16 bp mRNA linear NACL--02-J18.gl Rice callus plasmid cDNA library sativa cDNA clone NACL--02-J18, mRNA sequence.
                                                                                                                                                                                                                                   μ
 Oryza sativa
                   Oryza sativa
                                                         CF327923.1 GI:33804096
                                                                           CF327923
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

El (bases 1 to 16)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was capped
with_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0;
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CF328223
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Best Local Similarity
Matches 16; Conserv
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NACL--03-A10.gl Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--03-A10, mRNA sequence.
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Fax: 82 31 321 6355
                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongVi University Yongin, Kyeongyi, Korea Tel: 82 31 330 6193
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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with oligoribonuclectides and then used as templates for
RT-PCR."
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Location/Qualifiers
                                                                                                                                                                                                            bhnahm@ggbio.com,
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                                                                                                                                                                                 Location/Qualifiers
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5.4e+02;
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CF333386/c
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                                                                     Pocus
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JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
                BQ590128 17 bp mRNA linear E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root cDNA clone 024-019-E19 3-PRIME, mRNA sequence. BQ590128
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Tel: 82
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
 BQ590128.1
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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CF333386.1 GI:33815044
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82 31 321 6355
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was cap with oligoribonucleotides and then used as templates RT-PCR."
                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                    methyltransferase overexpression line."
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GI:26119711
                                                                                                                                                                                                                                               100.0%;
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Pred. No. 5.4e+02;
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Pred. No.
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5.4e+02;
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plasmid cDNA
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CF294668
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophytales; Amaranthaceae; Beta.

1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
                                                                                                                                                                                                                                                         17 bp mRNA linear EST 1.30DGS--04-E17.gl Rice leaf plasmid cDNA library I (30DGS) sativa cDNA clone 30DGS--04-E17, mRNA sequence.
CF294668
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                               Oryza sativa
Oryza sativa
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                      CF294668.1 GI:33663701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 17 Std Error: 0.00 Plate: 19 row: E column: 19 Seg primer: T7; GTAATACGACTCACTATAGGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet go Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Weisshaar B
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Beta vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pcWVSPORT6; Site 1: Sall; Site 2: Not!;
/note="Vector: pcWVSPORT6; Site in Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not!, primer sites and
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/lab_host="EMDH10B"
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/clone="024-019-E19"
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/mol_type="mRNA"
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100.0%; Pred. No. 6.2e+02;
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Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., L.

Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 bp mRNA linear EST 14-AUG-: 30DGS--06-C17.bl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-C17, mRNA sequence. CF295988
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                                                                                                                                                                                                                                                               Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhna
Location/Qualifiers
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Oryza sativa
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Location/Qualifiers
1. .17
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Contact: Nahm B.H.
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/clone="30DGS--04-E17"
/tissue_type="lasf"
/tissue_type="lasf"
/dev_gtage="30 days after germination"
/lab_host="E.coli DH10B"
/clone lib="R.coli DH10B"
/clone lib="R.fice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capp
with oligoribonucleotides and then used as templates f
RT-PCR."
/dev stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
RT-PCR."
                                                                                                                                                         /organism="Oryza Bativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                  'tissue_type="leaf"
                                                                                                                                        clone="30DGS--06-C17"
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                                                                                                                                                                                                                                                                                       bhnahm@bio.myongji.ac.kr
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1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J.,
Song,S.I., Kim,J.K., Kim,Y.-K. a)
                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                     Oryza sativa
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82 31 330 6193
82 31 321 6355
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
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/cultivar="Nackdong"
/db xref="taxon:4530"
/db xref="taxon:4530"
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoKI; mENA was capped with oligoribonucleotides and then used as templates for RT-pCR."
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Location/Qualifiers
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100.0%; Pred. No.
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 and Nahm, B.H.
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                 Lee, T.H.,
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(7LEAF) Oryza
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                   Shin, Y.C.,
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CF302447
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JOURNAL
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Best Local
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TITLE
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COMMENT
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Matches 16; Conserv
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideae; Oryzeae; Oryza.
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1 (bases 1 to 17)
1 (bases 1, Jun, K.M., Cheong, P.J., Kim, M.J., Le Kim, J.S., Jun, K.M., Kim, Y.-K. and Nahm, B.H. Song, S.I., Kim, J.K., Kim, Y.-K. and Rice ESTs
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Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bhnahm@ggbio.com,
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/organism="Oryza sativa"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-07-P11"
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/dev_stage="7 days after germination"
/dev_stage="7 days after germination"
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/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was_capped
with_oilgoribonucleotides_and_then_used_as_templates_for_
pr._bcp."
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/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--01-K24"
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Pred. No.
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(7LEAF) Oryza
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RESULT 1250
CF336950
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Best Local Similarity
Matches 16; Conserv
                                                 ORGANISM
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                                                                                     CF336950.1 GI:33822280
EST.
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                             Oryza sativa
                                                                                                                                             JMT--07-D04.gl AtJMT-overexpressing transgenic rice library (JMT) Oryza sativa cDNA clone JMT--07-D04, n
                                                                 Oryza sativa
                                                                                                                                                                                      CF336950
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
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CF313013.1 GI:33684774
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                                                                                                                                                                                                                                                                                                                bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage=14 days after germination"
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/clone lib="ABF3-overexpressing transgenic rice plasmid
/clone library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
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/clone="ABF--08-P19"
/tissue_type="leaf"
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5. 6.2e+02;
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6.2e+02;
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.Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                     Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 bp mRNA linear EST 15-AUG-2: 7LEAF--04-I24.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-I24, mRNA sequence.
                                                                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
Oryza sativa
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Figure MyongJi University
                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="14 days after germination"
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/db_xref="taxon:4530"
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/tlssue_type="leaf"
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; Pred. No.
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CF311668 19 bp mRNA linear EST 15-AUG-2003
ABF--07-A05.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.
CF311668
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech I of Bioscience and Bioinformatics, MyongJi University
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                       /dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
|mol_type="mRNA"
|cultivar="Nackdong"
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'clone="ABF--03-008"
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3. 7.9e+02;
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16; Conserv
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Oryza sativa
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EST.
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                                               Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                 Contact: Nahm B.H.
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1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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HD--10-C14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, of Bioscience and Bioinformatics,
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                          of Bioscience and Bioinformatics,
                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                         Ehrhartoideae; Oryzeae; Oryza.
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82 31 321 6355
1: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
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/db xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 1; L
Pred. No. 7.9e+02;
                              bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                MyongJi University
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                                                                                                                                                                                                                                                                                                                                  Shin, Y.C.,
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(7LEAF) Oryza EST 15-AUG-2003

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Query Match
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Matches 16
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF325356 19 bp mRNA linear EST 18-AUG-2003
JMT1--03-A08.91 AtJMT-overexpressing transgenic rice lambda phage
CDNA library (JMT1) Oryza sativa CDNA clone JMT1--03-A08, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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                                                Similarity
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                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com, bhn
Location/Qualifiers
                                                                                                         /dev_stage="14 days after germination"
/lab_host="E_coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
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/knoI; cDNA was inserted into landa Uni-ZAP XR vector at 5
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="JMT1--03-A08"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                      /cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli_DH10B"
/clone_lib="05HDAC1-overexpressing transgenic rice_plasmid
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mol_type="mRNA"

cultivar="Nackdong"
                                              100.0%;
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100.0%; Pred. No. 7.9e+02;
                                              0.2%; Score 16; DB 1; L
100.0%; Pred. No. 7.9e+02;
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                           0
                         Mismatches
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                                                                  Length 19;
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TITLE
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AUTHORS
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ORGANISM
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AUTHORS
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VERSION
KEYWORDS
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CF299570
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CF330490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%;
Best Local Similarity 100.0%;
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1 (bases 1 to 20)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                         Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                               NACL--06-D16.b1 Rice callus plasmid cDNA library
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Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                          sativa cDNA clone NACL--06-\overline{\text{D16}}, mRNA sequence. CF330490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF299570 20 bp mRNA linear 7LEAF--03-K09.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--03-K09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF299570.1 GI:33671331
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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/cullivar="Nackdong"
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a; Poales; Poaceae;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lo

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence. CF282313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF282313 21 bp mRNA linear EST 14-AUG-20
14ETL--09-M08.gl Rice etiolated leaf plasmid cDNA library (14ETL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae;
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82 31 321 6355
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice_callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with_oligoribonucleotides and then used as templates for
                                                                               /note="Vector: pCR4-TOPO; with oligoribonucleotides
                                                                                                                                                                   /clone="14ETL--09-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/mol_type="mRNA"
/cultivar="Nackdong"
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clone="NACL--06-D16"
                                                                                                                                (14ETL)
                                                                                                                                                                                                                                                          db_xref="taxon:4530"
0.2%;
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                                                                                                                                                  _lib="Rice etiolated leaf plasmid cDNA library
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  Score 16;
Pred. No.
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  DB 1; L
9.7e+02;
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8.8e+02;
hes 0; Indels
                                                                                    Site_1: EcoRI; mRNA was capped and then used as templates for
                   Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Nouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ341108 21 bp DNA linear GSS 29 1M0073014F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0073014 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0073 row: O column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polyme
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Location/Qualifiers
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMM42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC1M0073O14"
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Matches Query Match Best Local

Similarity

100.0%; \*\*

Score 16; DB Pred. No. 9.70; Mismatches

DB 1; 9.7e+02;

Length 21; Indels

0;

Gaps

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Conservative

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Query Match
Best Local Similarity
Watches 16; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0232 row: M column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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GSS.
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                                                                                                                                                         /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resource)/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and solicated for amnicillin resistance "
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/strain="C57BL/6J"
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                                                                                                                                                selected for ampicillin resistance."
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0035 row: P column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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/lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/mol_type="qenomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DNA"
strain="C57BL/6J"
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Length 22; Indels

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ilarity 100.0%; Pred. No. 9.7 Conservative 0; Mismatches

0.2%; Score 16; DB 1; L00.0%; Pred. No. 9.7e+(

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RESULT 1262
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                                                                                                                                                                                                                                                                                 Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uranyi46 RNA linear EST 18-AUG-20
JMT--03-F05.91 ALJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-F05, mRNA sequence.
CF334146
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
                        Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                I (bases 1 to 23)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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University of Kentucky
101 Morgan Building, Universi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence tags from Pneumocystis carinii Unpublished (2000)
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Smulian, A.G., Arnold, J., Weise, M., W
Edman, J.C., Kovacs, J. and Cushion, M.
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Location/Qualifiers
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Kyeonggi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                details see www.uky.edu/Project/Pneumocystis/"
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/db_xref="taxon:4754"
/lab_host="E._coli"
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                                                                                                                                                                                                                                    Lee, T.H.,
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AZ330773/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ330773 23 bp DNA line 1M0056008F Mouse 10kb plasmid UUGCIM library Mu clone UUGC1M0056008 F, genomic survey sequence. AZ330773
                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0056 row: O column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welse,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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GSS.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
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Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--03-F05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="A-CMT-overexpressing transgenic rice
cDNA library (JMT)"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                               'sex="Male"
                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0056008"
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RESULT 1266
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AU257474/c
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Best Local S
Matches 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
  CF327904
                                                                                                                                                                                                                                                                                                                                                                                                    Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 24)
Kato,K. and Matoba,R.
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AU257474
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-743-72-5589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of expressed sequence tags from mouse brain
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                                                                                                                                          TTTGTTTAAGAAGAAAAATGAAAC 3294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                         /tissue_type="brain"
/clone_Tib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                     clone="BED0010682"
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Pred. No. 1.2e+03;
0; Mismatches 5
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EST 18-AUG-2003
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                  84112,
Tel: 8
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhaussrn, A. and Wright, D., Weiss, R.
                                                    University of Utah
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                           1M0011E06F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0011E06 F, genomic survey sequence.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                   Unpublished (2000)
                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                            Contact: Robert B.
                                                                                                                                                     plasmid inserts
                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTTCTGTTTGTGAATAAGGC 6490
801 585 5606
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                                      USA
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/[clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capwith oligoribonucleotides and then used as templates RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"
/clone="NACL--02-J06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 1.2e
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Best Local Similarity
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Insert Length: 10000 Std Error:
Plate: 0011 row: E column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)
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AZ349008.1 GI:10428245
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                                                                                                                    University of Utah University of Utah
                                                                                                                                                                      Contact: Robert B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                          USA
ddunn@genetics.utah.edu
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                                                                                                 Biomedical
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 1.2e+03;
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                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Mus musculus
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                                                                                                                                                            Unpublished (2000)
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male
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clone="UUGC1M0085013"
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                                                                                                                            Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a Cloned population of Trypanosoma brucei (TREU927/4 GUTTAT 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                           Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M.A. and Barrell, B.G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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T. brucei sheared genomic DNA
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                                                                                                                                                                                                                                                             nh1@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/db_xref="taxon:10090"
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A clone 155f12, reverse sequence,
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24
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NACL--01-E15.g1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--01-E15, mRNA sequence.
CF326989
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   bhnahm@ggbio.com,
                                                                                                                                                        /mol_type="mRNA"

/ cultivar="Nackdong"
/db_xref="taxon:4530"
/db_cref="taxon:4530"
/clone="NaCL--01-E15"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice_callus_plasmid_cDNA_library_(NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="155f12"
                                                                                                                                                                                                                                                                                                                                                            organism="Oryza sativa"
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100.0%; Pred. No.
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                                                                                         Score 16; DB 1;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                   bhnahm@bio.myongji.ac.kr.
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RESULT 1272 TA321G11P

LOCUS TA321G11P 26 bp DNA linear GSS 13-DE DEFINITION T. brucei sheared genomic DNA clone 321g11, forward sequence,

GSS 13-DEC-2000

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
                                                                                                                                                                     Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                 Takeuchi, I., Kohara, Y. and Tanaka, Y. Population analysis of cDNAs from unicellular
                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum Dictyostelium discoideum
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                                                              Email: hideko@biol.tsukuba.ac.jp
                                                                                                                                                     University of Tsukuba
                                                                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                                                               stages of Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                             Urushihara, H., Morio, T., Saito, T.,
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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/strain="TREU927"
/organism="Dictyostelium discoideum"
                                         Location/Qualifiers
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Pred. No. 1.4e+03;
0; Mismatches 5
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R59382/c
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JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R59382
R59382
Yh17e07.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:37726 3' similar to gb:M65131 METHYLMALONYL-COA MUTASE
                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov) for Trace considered overall poor quality Possible reversed clone: polyT not found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R59382
R59382.1 GI:830077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAACAAAACAGAATGAGGTGGG 7000
                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 1.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:37726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:44689"
/clone="VSF623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
                                                                                                                                                                                                              'sex="female"
                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 1.4e+03;
0; Mismatches 5
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RESULT 1276
CF298134/c
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CF332296/c
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JOURNAL
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                               CF298134 19 bp mRNA linear TLEAF--01-G09.gl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--01-G09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 32)
1 (kim.J.S., Jun.K.M., Cheong.P.J., Kim.M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)
                                                                                                  CF298134.1 GI:33669895
EST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF332296 32 bp mRNA linear EST MACL-.08-M01.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL-.08-M01, mRNA sequence. CF332296 CF332296.1 GI:33812816 EST.
                                                              Oryza sativa
                                                                                Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, C of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                       TCAGAAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="NACL--08-M01"
/clssue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                            79.28;
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Pred. No. 1.5e+03;
0; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                          Score 16;
Pred. No.
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, MyongJi University
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(7LEAF) Oryza
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CF298472
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Best Local Similarity
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CE 1 (bases 1 to 19)

RS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

AL Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbbb.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.

Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Unpublished (2003)
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/organism="Oryza sativa"
/mol type="mRNA"
/mol type="mRNA"
/culTivar="Nackdong"
/culTivar="Nackdong"
/db xref="taxon:4530"
/clone="71EAF--01-001"
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/dev_stage="7 days after germination"
/lab host="E.coli DH10B"
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/clone_Tib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Pred. No. 8.5e+02;
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Insert Length: 10000 Std Erro
Plate: 0080 row: F column: 06
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080F06 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwp42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                         musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT-PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 8.5e+02;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0354 row: A column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ509929
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC1M0354A07"
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AZ611602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0438 row: G column: 03
Seg primer: CGTIGTARAACGACGGCCAGT
Class: plasmid ende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 bp DNA linear GSS 13-DEC-20 1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0438G03 F, genomic survey secuence AZ611607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 19.
Location/Qualifiers
          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMV42Nr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www_jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWn22 (gil 4732114 | gb| AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and salected for ampicillin resistance "
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and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="UUGC1M0438G03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 8.5e+02;
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AZ775624/c
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errr
Plate: 0008 row: E column: 0:
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Unpublished (2000)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[473214]gb[AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="Male"
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0.2%; Score 15.8;

DB 1;

Length 19;

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REFERENCE
AUTHORS
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AZ786336
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                   Query Match
Best Local
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  l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ786336

19 bp DNA linear GSS 16-FEB-200200031H17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0031H17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: H column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ786336.1 GI:12923992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTTTTTTTTTTGT 4485
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801 585 7177
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 19.
                                                                          Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host "E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pW942nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UUGC2M0031H17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                   0.2%;
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Rodentia;
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Score 15.8; DB 1;
Pred. No. 8.5e+02;
0; Mismatches 2;
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                                         Length 19
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CF331733/c
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JOURNAL
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Best Local Similarity
Matches 17; Conserv
                                                             TITLE
                                         JOURNAL
                                                                                                         AUTHORS
                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                      20 bp mRNA linear EST 18-AUG-2003 MACL-07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--07-P15, mRNA sequence.
CF331733
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S25H10 AGS-1 Pneumocystis
AW333777
                                                  1 (Dases 1 to 20)
1 (Dases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Kim,J.S., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Song,S.I., Kim,J.K., Kim,Y.-K. and Rice ESTs
                                                                                                                                              Oryza sativa
Guraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edman, J.C., Kovacs, J. and Cushion, M. Expressed sequence tags from Pneumocystis carinii Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pneumocystis carinii
Pneumocystis carinii
                     Large-scale Sequencing Analysis
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         School of Biological Sciences
University of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 20)
Smulian, A.G., Arnold, J., Weise, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW333777.1 GI:6830134
                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                             CF331733.1 GI:33811693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Staben C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 Morgan Building,
10506-0225, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTTTTTTTTTTTTT 4482
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  and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: P. carinii organisms (3x10e9) from a single rat (59-1 sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pneumocystis
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="taxon:4754"
/lab_host="E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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Pred. No. 9.5e+02;
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AZ345710/c
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                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 05
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                        84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 20)
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AZ345710.1 GI:10424947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                            308,
                                                                                                                                                                                                                              quality sequence stop: 20. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
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/clone="MACL--07-P15"
/clone="MACL--07-P15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0080H05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                        sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%;
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Pred. No. 9.5e+02;
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AZ313243
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                                                                                                                                                                                                                                                               source
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0029 row: H column: 16
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 21.
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                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse_10kb_plasmid_UUGCIM_library" /note="Vector: pwD42arv, Purified_genomic_DNA_from I musculus_C57BL/6J (male) was obtained_from the Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                              clone="UUGC1M0029H16"
                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                        sex="Male"
                                                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                                                                                      organism="Mus musculus"
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Pred. No. 9.5e+02;
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AZ818565/c
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Best Local Similarity 89.5%;
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                                                                                                                                                                                                                                                                                                                                                         High
                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: K column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 21)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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Location/Qualifiers
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse_10kb_plasmid_UUGCIM_library"/note="Vector: pw042nv; Purified_genomic_DNA_from M.musculus_C57BL/6J_{male} was obtained_from the Jackson
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                                                                                                                                                                                                   /mol_type="genomic DNA"
                                                                                                                    sex="Male"
                                                                                                                                                  clone="UUGC2M0088K10"
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Laboratory Mouse DNA Resource

Query Match Best Local

l Similarity 17; Conserv

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Score 15.8; DB 1; Pred. No. 1.1e+03; 0; Mismatches 2;

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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Genomics and Genetics Institute, Cof Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF318882.1 GI:33690643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF318882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HD--09-C23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDlbrary (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGTTTTTTTTTTTTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 22
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                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--09-C23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                  derived
line."
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                  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Pred. No. 1e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GreenGene Biotech Inc.; Division , MyongJi University
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AZ771221/c
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VERSION
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  Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tal: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0573 row: A column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ771221 23 bp DNA linear GSS 16-FEB-200 1M0573A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0573A16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 23)
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  Conservative
                                                                                                Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 bb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse_10kb_plasmid_UUGCIM_library"/note="Vector: pWp42nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male) was obtained_from_the_Jackson_musculus_C57BL/6J_(male) was obtained_from_the_Jackson_musculus_C57BL/6J_(male)
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0573A16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'sex="Male"
                    0.24;
  0; Mismatches
                          Score 15.8; DB 1
Pred. No. 1.2e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
                                                    DB 1; Length 23;
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4460 GGACTTTTTTTTTTTTT 4478

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6004 GGAGGGTTTCTGGCATTTT 6022

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AZ314206
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                                                     Query Match
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Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0030 row: H column: 19
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ314206 24 bp DNA linear GSS 29-SEP-200
1M0030H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0030H19 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)
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                                                                                                  Laboratory Mouse DNA Resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42Tvr, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC1M0030H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                       0.2*;
Score 15.8; DB 1;
Pred. No. 1.3e+03;
0; Mismatches 2;
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                                                  Length 24;
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Best Local Similarity
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                         4405 TTTACAAAAATGAATTTTT 4423
23
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: M column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss University of Utah Genome University of Utah
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CACACAGGAAACAGCTATGACC
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Mammalia; Eutheria; Rodentia;
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801 585 7177
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Location/Qualifiers
                                                                                              Conservative
                                                                                                                                                                                                                                                       was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NAA and transformed into
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                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
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/clone="UUGC1M0080M05"
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/strain="C57BL/6J"
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                                                                                                                0.2%;
                                                                                              0; Mismatches
                                                                                                                  Score 15.8; DB 1;
Pred. No. 1.3e+03;
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UUGC1M library Mus musculus genomic
c survey sequence.
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24 l
1M0535L19F Mouse 10kb plasmid
clone UUGC1M0535L19 F, genomic
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Insert Length: 10000 Std Error:
Plate: 0535 row: L column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 24)
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AZ658569.1 GI:11795715
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                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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0.2%;
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  Score 15.8;
Pred. No. 1.
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smid UUGC1M library Mus musculus genomic
1.3e+03;
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AW327923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
Genomics and Genetics Institute, (
of Bioscience and Bioinformatics,
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                           Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                             CF291968 27 bp mRNA linear 14ROOT--02-J21.bl Rice root plasmid cDNA library sativa cDNA clone 14ROOT--02-J21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Edge BioSystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLCM0029 row: M column: 16
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AW327923
                                                                                                                    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                          CF291968.1 GI:33661001
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Seq primer: -21M13 forward primer
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1 (bases 1 to 27)
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                                                                                                   Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_3"
/note="Organ: Lymph; Vector: pOTB7a; Library prepared
Edge BioSystems."
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/clone="IMAGE:2847159"
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/mol_type="mRNA"
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; Pred. No. 1.6e
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1.6e+03;
7;
                                                        GreenGene Biotech I
, MyongJi University
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                                                                          Biotech Inc.; Division
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Best Local Similarity
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                                   4013 AAATGAGAAAAAAGAGAGAAAAACAAAA 4039
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF299084 27 bp mRNA linear EST 15-AUG-20
7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--02-P02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
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                                                                                                                                               /tissue_type="leaf"
/dev_stage="7 days after germination"
/lab host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOP0; Site_1: EcoR1; mRNA was cap
with_oligoribonucleotides and then used as templates
                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
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/cultivar="Nackdong"
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1. .27
                                                                                                                                                                                                                                                                                 /db_xref="taxon:4530"
/clone="7LEAF--02-P02"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--02-J21"
                                                                                         0.2%;
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Pred. No. 1.6e
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CF329725/c
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ARCL--05-C12.bl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-C12, mRNA sequence.

CF329725
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Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
                                                                                                       1 (bases 1 to 27)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                    Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                      Oryza sativa
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Similarity 74.1%;
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/culTivar="Nackdong"
/culTivar="Nackdong"
/db xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
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/dev stage="proliferated callus on 2N6 media for 30 days"
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/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Location/Qualifiers
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Pred. No. 1.6e+03;
0; Mismatches 7;
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CF335229/c
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JMT--04-NO8.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
Library (JMT) Oryza sativa cDNA clone JMT--04-NO8, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Large-scale Sequencing Analysis Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
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                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--04-N08"
                                                                                                                                          /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
                                                                                  /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxy1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; with oligoribonucleotides
                                                                 methyltransferase overexpression line."
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/lab host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="Nackdong"
/db_xref="taxon:4530"
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|mol_type="mRNA"
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Pred. No. 1.
    Score 15.8; DB 1;
Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GreenGene Biotech Inc.; Division, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6e+03;
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                     Length 27;
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: CPlate: 0168 row: K column: 04
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S.
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Fax: 801 585 7177
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/note="Wector: PW042nv; Purified genomic DNA from M. musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant,/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
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/strain="C57BL/6J"
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Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: K column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                          Conservative
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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74.1%;
                                                                                                                              Score 15.8; DB 1; Length 27; Pred. No. 1.6e+03;
                                                                                                       Mismatches
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Mismatches

Pred.

Score 15.8; DB 1; Pred. No. 1.6e+03;

Length 27;

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Query Match Best Local Similarity

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RESULT 1302
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Mouse whole genome scaffolding with paired end reads from 10kb
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0357 row: E column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (2000)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0369 row: E column: 24
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Contact: Robert B.
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AZ580921.1 GI:11695417
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1M0369E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0369E24 F, genomic survey sequence.
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/strain="C57BL/6J"
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clone="UUGC1M0369E24"
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                                                                                                                          Score 15.8; DB 1;
Pred. No. 1.6e+03;
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AUTHORS
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Fax: 801 585 7177
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0445 row: E column: 17
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University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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USA
                                                                                                     Conservative
                                                                                                                                                                                            /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114/gb/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                           74.18;
                                                                                                                             Score 15.8;
Pred. No. 1.
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20; Conserv
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Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 12
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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'strain="C57BL/6J"
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Pred. No. 1.6e+03;
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linear

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DEFINITION AZ809295 RESULT 1307

AZ809295 27 bp DNA linear GSS 20-FEB-200 2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

GSS 20-FEB-2001

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REFERENCE
AUTHORS
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymicleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone="UUGC1M0474011"
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RESULT 1308
TA355B06P
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Matches 20; Conserv
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TA355B06P 27 k
T. brucei sheared genomic DNA
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0073 row: B column: 15
Seq primer: CGTTGTAAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 27.
Location/Qualifiers
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AZ809295.1 GI:12975450
GSS.
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pDNA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil XIIO-Gold (Stratagene) cells and selected for a midillia vecities of stratagene) cells
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/clone="UUGC2M0073B15"
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/strain="C57BL/6J"
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Pred. No. 1.
                                clone 355b06, forward
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AZ941721/c
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Best Local Similarity 74.1%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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AL493923.1
GSS.: }::3.*.
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                                                                                                                                University of Utah (University of Utah Rm. 308, Biomedical
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 27)
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                           plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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Location/Qualifiers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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1 (bases 1 to 27)
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="355b06"
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1M0220B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0220B08 R, genomic survey sequence
                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 27)
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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/strain="C57BL/6J"
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                                                                                                                   Polymers Research Bldg.,
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Pred. No. 1.6e+03;
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Best Local Similarity
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0262 row: C column: 1;
                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                          University of Utah Genome Cen
University of Utah
Rm. 308, Biomedical Polymers
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0220B08"
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Matches 20
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Unpublished (1999)
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/db xref="taxon:9606"
/db xref="taxon:9606"
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/tissue_type="uterus"
/dev_stage="adult"
/lab_host="OH108"
/clone_lib="586 (synonym: hutel)"
/note="Vector: pSport1; Site_1: Not1; Si
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/mol_type="mRNA"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
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Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hutel) Homo
                                                                                                                                                                                                                                                                                                                                                                                                             Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
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    Site_2: SalI/MluI"
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                   CP337400 28 bp mRNA linear EST 18-AUG-2003 JMT--07-N04.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-N04, mRNA sequence. CP337400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 28)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                     CF337400.1 GI:33823200
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HD--13-I23.gl OsHDACl-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--13-I23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                          Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--13-I23"
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Pred. No. 1.7e+03;
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Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse,Whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
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Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0303 row: L column: 24
                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0303L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0303L24 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ481286.1 GI:10642351
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                                                                                                                                                                         308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus (house mouse)
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82 31 330 6193
82 31 321 6355
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                                                                                                                                                       USA
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                                                                                                                                                                       Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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cultivar="Nackdong"
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                                                                                                                                                                    Polymers Research Bldg.,
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Pred. No. 1.7e+03;
0; Mismatches 7;
                                                              Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chiasoe, S., Dietrich, N., Kucaba, T., Lacy, M., Le, M., Le, N., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Markins, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Markins, T., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756352
T56352
T8636-PEB-199
Yb34C09.s1 Stratagene fetal spleen (#937205) Home sapiens cDNA
clone IMAGE:73972 3' similar to similar to gb:541458 ROD
CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN),
Email: est@watson.wustl.edu
High qality sequence starts: 1
High qality sequence stops: 1
                                                                                                                                         Washington University Scho 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                             8889549
                                                                                                                                                                                                                                                                                                                                          and Marra, M.
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                                                                                                                                                                                                   Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fomo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARABABABABABABABABABABACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/Clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PW827uv; Durified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="UUGC1M0303L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                            School of Medicine way, Box 8501, St. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 1;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 28;
                                                                                                                                               Louis,
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REFERENCE
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AZ825156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: N column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                              308,
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                                                                                                                                 quality sequence stop: 29.
Location/Qualifiers
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/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg.,
                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0100N08"
                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="MAGE:73072"
/rissue_type="fetal spleen"
/dev_stage="fetal"
/dev_stage="fetal"
/lab_host="SOLR_cells (kanamycin_resistant)"
/lab_host="SOLR_cells (kanamycin_resistant)"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"

mol_type="mRNA"
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Pred. No. 1.7e+03;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
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BQ583967/c
LOCUS
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AUTHORS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                            Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seg primer: T7; GTAATACGACTCACTATAGGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 29)
1 (bases 1 to 29)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ583967.1 GI:26113544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
/tissue_type="inflorescence"
/lab_host="EMDH10B"
                                                                                  /db_xref="GABI:182728"
/db_xref="taxon:161934"
                                                                                                                                                                                                  organism="Beta vulgaris"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                    Socation/Qualifiers
                                                             clone="024-004-B01"
                                                                                                                                                                       cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                             ine) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta vulgaris
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SOURCE

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                                          Matches
                                                             Query Match
Best Local S
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4018 AGAAAAAGAGAGAAAACAAAATGTTA 4044
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                                                                                                                                                                                                                                                                                                                                                                                         Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
Ball Clones with suffix qlc are reverse primer reads starting at
end of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hall N
Pathogen Sequencing Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Hippoboscoidea; Glossinidae; Glossina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 4 (10), R63 (2003)
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                                                             Similarity
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                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not!;
/nota library from sugar beet, llbrary provided by KWS
cDNA library from sugar beet, llbrary provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing granted in the context of the GAB1-Beec project, local PI: Dr. Katharina Schneider, coordinator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Sequencing granted in the context of the GABI-Beet
                                                                                                                                                                                       /clone="Tse17d12_plc"
/tissue_type="adult infected gu
/tione_lib="Glossina morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RZPD/GABI-Primary database: http://gabi.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                   /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
                                                                                                                                                                                                                                                          sub_species="morsitans"
db_xref="taxon:37546"
                                                                                                                                                  note="country: Zimbabwe;
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                                    ; Score 15.8; D; Pred. No. 1.8e
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one Tse17d12_plc, mRNA seq
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AZ326012
Matches
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1M0048A19R Mouse 10kb plasmid UUGCIM library Mu
clone UUGC1M0048A19 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0048 row: A column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 32)
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Conservative
                                                                                         http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone 11b="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWR42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0048A19"
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                        74.1%;
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Genome Center
0;
                        Score 15.8; DB 1;
Pred. No. 1.9e+03;
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Mismatches
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                                                Length 32;
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42 bp DNA linear GSS 16
1M0571B19F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0571B19 F, genomic survey sequence.
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                    SSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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                    plasmid inserts
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AL483993.1 GI:11849953
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="264b08"
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Pred. No. 1.9e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 GCAGGCAGGCAGGCAGGCAGGCAGGCAGGCA 8
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing Submitted (10-DEC-2000) Trypanosoma brucei genome Campus, Hinxton, project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
AL497383
                                                                                                                                                                                                                                                                                                                                                                                            TA303G05P
                                                                                             Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Homelville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                             Trypanosoma
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High quality sequence stop: 42.
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Insert Length: 10000 Std Error:
Plate: 0571 row: B column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84112,
                                                                                                                                                                                                                                                                                                                                                                                          brucei sheared genomic
                                                                                                                                                                      (bases 1 to 22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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AA999803
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Best Local Similarity 81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAAAAAAAAAGAAAAAAAA 22
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4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
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National Cancer Institute, Cancer Genome Anat
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Br2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
                                                                              /clone="IMAGE:1607911"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                 B
                                                                                                                                                                                                      organism="Homo sapiens"
|mol_type="mRNA"
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Pred. No. 1.2e+03;
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AZ471736 22 b
AZ471736 22 b
IM0286112R Mouse 10kb plasmid
clone UUGC1M0286112 R, genomic
AZ471736
AZ471736.1 GI:10629957
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CF300339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Oryza sativa
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/clone="7LEAF-04-L05"
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/dev stage="7 days after germination"
/dev stage="7 days after germination"
/lab_host="E_coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Ec RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI_CGAP_Brl.1. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 1.2e+03;
                                      genomic survey sequence.
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                                                        22 bp DNA linear GSS 04-OCT-200 mid UUGC1M library Mus musculus genomic
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Tel: 801 585 5606
Fax: 801 585 7177
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AZ592068 22 bp DNA linear GSS 13-DEC-200 1M0402H08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0402H08 R, genomic survey sequence.

AZ592068 AZ592068 GI:11714258 GSS.
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Insert Length: 1000 Std Error: 0.00
Plate: 0286 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
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/mol_type="qenomic nwa"
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  Mus musculus (house mouse)
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Insert Length: 10000 Std Error: (
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Location/Qualifiers
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University of Utah Genome Center
University of Utah
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/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.iax.or//nesource
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/strain="C57BL/6J"
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                                                   GI:11755941
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Pred. No. 1.2e+03;
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TA189G04P/c
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18; Conserv
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                                                                                                                      T. brucei sheared genomic genomic survey sequence.
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Fax: 801 585 7177
Email: 804 585 7177
Email: 6dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: I column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mahmoud,M. Mense whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
       Trypanosoma brucei
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1 (bases 1 to 22)
                              Trypanosoma brucei
                                                                           AL477750.1 GI:11841701
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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strain="C57BL/6J"
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Contact: Robert B. Wo
University of Utah G
University of Utah
Rm. 308, Biomedical I
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="189g04"
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/mol_type="genomic DNA"
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Pred. No. 1.2e+03;
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0510 row: O column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse, whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
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AZ645254.1 GI:11774572
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                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAAAAAGAAAAAAAA 2
                                                                                                                                                                                                                                                                         308,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 1.3e+03;
                                                                                                                               Std Error: 0.00
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UUGC1M library Mus musculus genomic
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RESULT 1332
AU012506/c
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AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     Genome Research Group
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morthyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU012506 23 bp mRNA linear EST 03-AU AU012506 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc06890, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 23)
Morinyo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
Schizosaccharomyces pombe (fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU012506.1 GI:3357415
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/clone="spc06890"
/clone="h minus"
/sex="h minus"
/clone lib="Schizosaccharomyces pombe late log phase cDNA"
/clone lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                          organism="Schizosaccharomyces pombe"
|mol_type="mRNA"
                                                                                                                                                                     db_xref="taxon:4896"
                                                                                                                                                                                                   /strain="972"
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/clone="UUGC1M0510005"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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Pred. No. 1.3e+03;
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AZ618720/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0450 row: O column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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23 bp DNA linear GSS 13-DEC-20:
1M0450019F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0450019 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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1 (bases 1 to 23)
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NNA adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0450019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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Pred. No. 1.3e+03;
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and transformed into

COMMENT

TITLE

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Query Match
Best Local Similarity
Matches 18; Conserv
                                                                          chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                 0.2%;
                   Score 15.6; DB 1;
Pred. No. 1.3e+03;
                                         Length
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REFERENCE AUTHORS RESULT 1334 AZ793326/c KEYWORDS SOURCE ACCESSION VERSION FEATURES COMMENT DEFINITION TITLE ORGANISM JOURNAL source 3622 СССТСССССТСССАСАСАССАСС 3643 Contact: Robert B. W. University of Utah Ge University of Utah Rm. 308, Biomedical I 23 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Eror: | Plate: 0046 row: B column: 04 Seq primer: CACACAGGAAACAGCTATGACC Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus 2M0046B04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic High quality sequence stop: 23. Tel: 801 585 5606 Fax: 801 585 7177 Unpublished (2000) plasmid inserts Mouse whole genome scaffolding with paired end reads from 10kb AZ793326.1 GI:12938168 clone UUGC2M0046B04 R, genomic survey sequence. AZ793326 lass: plasmid ends GGGGGGGGGGGGGAGG 2 (bases 1 to 23) musculus (house mouse) USA 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson aboratory Mouse DNA Resource /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-" clone="UUGC2M0046B04" mol\_type="genomic DNA'strain="C57BL/6J" ocation/Qualifiers sex="Male" db xref="taxon:10090" organism="Mus musculus" Genome Center Weiss Polymers Research Bldg., Std Error: 0.00 23 bp DNA linear 20 S. 2030 E., GSS 16-FEB-2001 Murinae; Mus. SLC, Ę þ

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RESULT 1335
AZ822888/c
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Best Local S
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Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: G column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ende
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Location/Qualifiers
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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Unpublished (2000)
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AZ822888.1 GI:12992796
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/cnote="Vector: PWD42nv; Purified_genomic_DNA_from_M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UUGC2M0096G06"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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Best Local Similarity
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University of Utah Genome Center
University of Utah
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High quality sequence stop: 23.
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Insert Length: 10000 Std Err
Plate: 0265 row: I column: 2
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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23 t
240265123F Mouse 10kb plasmid
210ne UUGC2M0265123 F, genomic
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pNP042 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="UUGC2M0265I23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:13855272
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Pred. No. 1.3e+03
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d UUGC2M library Mus musculus
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AZ626101/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 bp DNA linear GSS 13-DEC-20(
1M0466J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0466J07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error:
Plate: 0466 row: J column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="B_Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM Tibrary"/note="Vector: pM942nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0466J07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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Pred. No. 1.3e+03;
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Query Match

0.2%;

Score 15.6;

DB 1;

Length 24;

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RESULT 1338
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ORGANISM
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VERSION
KEYWORDS
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                                                                                                                                                                                                        DEFINITION
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AW246443
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                       4018 AGAAAAAAGAGAGAAAACAAAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 24)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 24)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                         AW246443

AW246443

AW24537.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2821537 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF281313.1
EST.
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                                                                                         Homo sapiens
                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                  AW246443.1 GI:6589436
                                                                                                                                                                    AW246443
                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4530"
/clone="148TL--08-F05"
/tissue_type="1e4f"
/dev_stage="14 days after germination"
/lab_host="E.coli_PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for TY-PCR "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (14ETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="Rice etiolated leaf plasmid cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.6; DB 1;
Pred. No. 1.4e+03;
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REFERENCE
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Best Local Similarity
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Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov

Email: Cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
CONSORTIUM (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center:
Vector
Trimming: cross match from University of Washingtion Genome Center:
PHRAP suite. Poly-T Identification: patkmatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4476 TTTTTTTTTGTCTTGAGACATGG 4497
Unpublished (1999)
Other ESTs: 2819212.5prime
Other ESTs: 2819212.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 24)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab Nost-"PH108 (phage-resistant)"
/lab Nost-"PH108 (phage-resistant)"
/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
/note-"Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: FOORI; CDNA made by Oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2821537"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/mol_type="mRNA"
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81.8%;
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Pred. No. 1.4e+03;
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Plate: LLCM1 row: A column: 5
High quality sequence stop: 10.
                                                                  /clone lib="NIH MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="small cell carcinoma"
/cell line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone llb="NIH MGC 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:2819212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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0.2%;
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FEATURES

S Query Match Best Local Matches 4018 AGAAAAAAGAGAGAAAACAAAA 4039 18; Similarity Conservative 81.8%; <u>.</u> Score 15.6; DB 1; Pred. No. 1.4e+03; Mismatches Length 24; Indels 0;

0

RESULT 1341 AZ404465 밁 DEFINITION 24 AGAAAACAGAGTGTAAAAAAA 3

ACCESSION VERSION KEYWORDS AZ404465 24 bp DNA linear GSS 03-OCT-200100172P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0172P09 R, genomic survey sequence. AZ404465.1 GI:10528394 GSS 03-OCT-2000

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

REFERENCE AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Contact: Robert B. University of Utah University of Utah plasmid inserts Unpublished (2000) Weiss Genome Center

COMMENT

TITLE

Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 84112, 308, USA Polymers Research Bldg., 0.00 20 . 2030 E., STC,

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JOURNAL COMMENT
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil, Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ404078 25 bp DNA linear GSS 03-OCT-20 1M0172J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0172J07 F, genomic survey sequence.
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0172 row: J column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AZ404078.1 GI:10528091
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                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                          University of Utah University of Utah
                                                                                                                                                                                                                            Contact: Robert
                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                              plasmid inserts
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                                                                                                                             USA
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                                                                                                                                                Biomedical Polymers Research Bldg.,
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clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 1.4e+03;
                          Std Error: 0.00
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hes 18; Conserv
NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Lunpublished (1999)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW249476.1 GI:6592469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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/clone="UUGC1M0172J07"
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/strain="C57BL/6J"
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Pred. No. 1.
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                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errr
Plate: 0493 row: G column: 18
                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus (bases 1 to 26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0493G18F Mouse 10kb plasmid UUGCIM library Muclone UUGC1M0493G18 F, genomic survey sequence.
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                                                                                                                                       Plate: 0493 row: G column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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Location/Qualifiers
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/clone lib="NXH_MGC_7"
/clone lib="NXH_MGC_7"
/clone lib="Iung; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Total ande by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(c). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:9606"
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/tissue_type="small cell carcinoma"
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Pred. No. 1.5e+03;
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CF298133/c
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/clone="UUGCLM0493G18"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note=""vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF298133 27 bp mRNA linear 7LEAF--01-G09.b1 Rice leaf plasmid cDNA library IJ sativa cDNA clone 7LEAF--01-G09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi |4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com, bhna
Location/Qualifiers
1. .27
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was cappe
with oligoribonucleotides and then used as templates fc
                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-G09"
                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korea
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                                                                                                                                                                                                                                                                                                                                                                                   bhnahm@bio.myongji.ac.kr
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer:murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly
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Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                     EX556508 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse27f04_plc, mRNA sequence.

EX556508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq
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                                                         BX556508.1 GI:33427768
                                                                                                                 BX556508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP Chicken Brain Library
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Similarity 81.8%;
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/db_xref="taxon:9031"
/clone="ROS059B09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Gallus gallus"
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Pred. No. 1.7e+03;
0; Mismatches 4;
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BX553095/c
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
                                                                                                                                                                                                                                                                   response genes
Genome Biol. 4 (10),
22881942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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School of Biological Sciences,
University of Wales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 4 (10), R63 (2003) 22881942
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Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 35)
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3' end.
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/clone="Tme27f04_plc"
/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans mo
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/mol_type="mRNA"
/c...b______
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                                                                                                                                                                                                                                                                                                          R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                     analysis of putative immune
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AW248574
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                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_ESTs: 2821096.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
AW248574
AW248574.1 GI:6591567
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 17)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW248574 17 bp mRNA linear EST 07-JAN-200 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       School of Biological Sciences,
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                                                                                                                                                                                                              e: LLCM5 row: O column: 17 quality sequence stop: 8.
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                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="small cell carcinoma"
/cell_lIne="MGC3"
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/db_xref="taxon:37546"
/clone="Tse127007_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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/mol_type="mRNA"
                                                           clone="IMAGE:2821096"
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Pred. No. 1.9e+03;
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BQ591181
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/clone lib="NIH MGC 7"
/clone "Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
CoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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E012715-024-017-H16-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.
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Plate: 17 row: H column: 16
Seq primer: T7; GTAATACGACTCACTATAGGGC
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Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: weisshaa@mpiz-koeln.mpg.de
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                                                                                                                                                                            /clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
/note="Vector: pcmvSpORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, lTbrary provided by KWS
cDNA library from sugar beet, lTbrary provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
b.schulz@kws.de; cloning sites SalI-NotI, primer sites
Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                                                                                                                                                                                                                                                                                                                                  /tissue_type="storage root"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Beta vulgaris"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:161934"
/clone="024-017-H16"
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/clone lib="NIH MGC 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="GABI:188932"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA Clone 024-017-C15 5-PRIME, mRNA sequence.
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Max-planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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                                                                                                Similarity
TTATTTTTTTTTTT 17
                                    TTTTTTTTTTTTTT 4480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : weisshaa@mpiz-koeln.mpg.de
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 17 Std Error: 0.00
17 row: C column: 15
imer: SP6; CATACGATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                      /clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Salte 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Salte 2: Not1;
cDNA library from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
bischulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                     Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de*
                                                                                                                                                                                                                                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Beta vulgaris"
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/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="storage root"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:161934"
/clone="024-017-C15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="GABI:188532"
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Pred. No. 7.8e+02;
0; Mismatches 1
                                                                                              Score 15.4; DB 1; Length 17; Pred. No. 7.8e+02;
                                                                         Mismatches
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SOURCE
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AUTHORS
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CF291802
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CF276637/c
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CF291802.1
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Query Match
Best Local Similarity
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                           I (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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Yongin, Kyeonggi, K
Tel: 82 31 330 6193
                                           of Bioscience and Bioinformatics, MyongJi University
                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="leaf"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 7.8e+02;
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                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conser
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Best Local Similarity
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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CF299997.1 GI:33671758
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Email:
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                                                                                                                                                                                                                               /organism="Oryza sativa"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Location/Qualifiers
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Location/Qualifiers
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/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/db xref="Nackdong"
/clone="14ROOT--02-G05"
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                                                  0.2%;
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Pred. No. 7.8e+02;
0; Mismatches 1;
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                                                                                                                     Score 15.4; DB 1;
Pred. No. 7.8e+02;
0; Mismatches 1;
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                                                                                                                                                                    Length 17;
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CF329285
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CF319075
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                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.2%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                  AUTHORS
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Oryza sativa
Oryza sativa
Oryza sativa
Oryza sativa
Oryza sativa
Oryza sativa
Spermatophyta; Viridiplantae; Streptophyta; Embryop
Spermatophyta; Magnollophyta; Liliopsida; Poale
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
1 (bases 1 to 18)
1 (hases 1 to 18)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnah
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1/ DP MRNA linear EST 15-AUG-2003 HD--09-H06.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence. CF319075
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m Ibrary} (HD)"
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/cissue_type="callus"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                     Embryophyta; Tracheophyta; a; Poales; Poaceae;
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18-AUG-2003

Lee, T.H.,

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REFERENCE
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                        organism="Oryza sativa"
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/cultivar="Nackdong"
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Score 15.4; DB 1;
Pred. No. 9.9e+02;
0; Mismatches 1;
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Pred. No. 8.8e+02;
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
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1M0244J19F Mouse 10kb plasmid UUGC1M library Mu
clone UUGC1M0244J19 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0244 row: J column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606 Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus muscuius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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AZ447251.1 GI:10599050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 19.
Location/Qualifiers
/lab host="B. Coli strain XL10-Gold, T1-resistant, P-"
/(alone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWn92 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC1M0244J19"
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UUGC1M library Mus musculus
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Matches Query Match Best Local

Similarity

0.2%;

Score 15.4; DB 1; Pred. No. 9.9e+02; 0; Mismatches 1

DB 1;

Length 19

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Conservative

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AZ316368/c
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0034 row: L column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errc
Plate: 0034 row: L column: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 20)
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Mus musculus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308,
                                                                   Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD2 (gi|4732114|gb|AFT29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the innert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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94.18;
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Score 15.4; DB 1;
Pred. No. 1.1e+03;
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mid UUGC1M library Mus musculus genomic
                       Length 20;
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Matches 16;

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AZ369092/c
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Query Match
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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
Plate: 0119 row: E column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ass: plasmid ends
                                                                                              Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC1M0119E01"
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                      0.2%;
                         Score 15.4; DB 1;
Pred. No. 1.1e+03;
                                                   Length 20;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                     AZ831993
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                                                                 1 (bases 1 to 21)
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,B., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                            21 bp DNA linear GSS 20-FEB-200
2M0112M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0112M01 F, genomic survey sequence.
AZB31993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF330439 21 bp mRNA linear EST 18-AU NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-C12, mRNA sequence.
                  plasmid inserts
Unpublished (2000)
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  Contact: Robert B. Weiss
                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                             Mus musculus (house mouse)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="NACL--06-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab host="E_coli DH10B"
/clone_lib="Rice_callus_plasmid_cDNA_library_(NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Nackdong"
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                  JOURNAL COMMENT
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AZ843343
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                          plasmid inserts
                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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7413 CAGCAGCAGCAGCA 7429
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                            AZ843343

21 bp DNA linear GSS 20-FEB-200
2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142K10 F, genomic survey sequence.
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                                                                                                                                                                                                                Mus musculus
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Insert Length: 10000 Std Error:
Plate: 0112 row: M column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                            Mus musculus (house mouse)
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Fax: 801 585 7177
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igh quality sequence stop: 21.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC2M0112M01"
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TA154D03P/c
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Best Local Similarity
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population
                                                                         Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errx
Plate: 0142 row: K column: 11
                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                   ĀL472971
ĀL472971.1 GI:11838244
                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                                                        nh1@sanger.ac.uk
                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TA154D03P
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                brucei sheared genomic DNA
                                                                                                                                                                                                                                                       (bases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclaotide kinase. Adaptor oligonuclaotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mo1
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strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC2M0142K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 1; Length 21; Pred. No. 1.2e+03;
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e 154d03, forward sequence,
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AZ764498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: K column: 04
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ764498 25 bp DNA linear 1M0560K04R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0560K04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to give a tight size distribution ( 4 kb). ..., ... The \nu + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ764498.1 GI:12879523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                              lass: plasmid ends
igh quality sequence stop: 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                     /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clones"UUGC1M0560K04"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGCIM_Ibrary"/note="Vector: pW042nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male) was obtained_from_the_Jackson_musculus_C57BL/6J_(male) was obtained_from_the_Jackson_musculus_C57BL/6J_(male)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="154d03"
                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                      'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Trypanosoma brucei"
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76.0%;
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Pred. No. 1.6e+03
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25
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1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 bp mRNA linear EST 15-AUG-2071EAF--03-L24.bl Rice leaf plasmid cDNA library II (71EAF) Oryza sativa cDNA clone 71EAF--03-L24, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
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  attaraaaaaaaaaaaaaaaaa
                                               ATGAGAAAAAGAGAGAAAACAAAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. col1 XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                              /cultivar="Nackdong"
/db xref="taxon:4530"
/cloine="7LEAF--03-L24"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/cloine lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                     76.0%;
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                                                                                           Score 15.4; DB 1;
Pred. No. 1.7e+03;
0; Mismatches 6
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Pred. No. 1.6e+03;
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                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

AL Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBlO 15A, B-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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AL482943.1 GI:11847403
GSS.
                                                              1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                      N29432
27 bp mRNA linear EST 05-JJ
yw86h10.sl Soares placenta Sto9weeks 2NbHP8tc9W Homo sapiens
clone IMAGE:259171 3' similar to gb:X64559 TETRANECTIN PRECUF
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The WashU-Merck EST Project Unpublished (1995)
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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T. brucei sheared genomic
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                 N29432.1 GI:1147952
                                                                                                                                                                                                                                                                                                                   (HUMAN);, mRNA sequence. N29432
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                                              Wilson, R.
                                                                                                                                                                                                                                                Homo sapiens (human)
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/strain="TREU927"
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N52529/c
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Best Local Similarity
Matches 19; Conserv
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wattson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N52529 27 bp mRNA linear EST 15-FEB-1996 yv35al2.sl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
                                                                                                                                        The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., E.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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N52529.1 GI:1193695
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seg primer: m13 -40 forward
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIN-1 (HUMAN);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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/mol_type="mRNA"
/db_xref="GDB:3888877"
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Pred. No. 1.8e+03;
0; Mismatches 6
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Best Local S
Matches 19
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                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4284 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1410
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R37697 28 bp mRNA linear EST 04-MAY-199 yf50c03.sl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:25521 3' similar to gb:J03040 SPARC PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 TCNAAAAAAAAAAAAAAAAA 1
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1 (bases 1 to 28)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                     Insert Length: 1410
Seq primer: -21m13
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK
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Location/Qualifiers
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                                                                                    quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="GDB:397868"
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/clone="IMAGE:244702"
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/mol_type="mRNA"
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/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:3793948"
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CF299294
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KEYWORDS
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Best Local (
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                                       4012 AAAATGAGAAAAAAGAGAGAAAACA 4036
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N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                        bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                           /dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded CDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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/clone="7LEAF--03-E04"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="IMAGE:25521"
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                                                                             Score 15.4; DB 1;
Pred. No. 1.8e+03;
); Mismatches 6;
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(7LEAF) Oryza
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BX567540/c
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                                                                                                                                                      CF297930 31 bp mRNA linear TLEAF--01-B17.gl Rice leaf plasmid CDNA library II sativa cDNA clone 7LEAF--01-B17, mRNA sequence. CF297930 CF297930.1 GI:33669691
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1 (bases 1 to 31)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., I
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                  Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UM
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Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
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Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 29)
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/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
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/sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Glossina morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="country: Zimbabwe;
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                        Lee, T.H.,
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(7LEAF) Oryza
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BF032851/c
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                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9592 row: b column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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19; Conserv
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Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BF032851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 32)
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: 82 31 330 6193
: 82 31 321 6355
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Location/Qualifiers
/tissue_type="adenocarcinoma"
/lab_host="pHiOB (phage-resistant)"
/clone_lib="NIH_MGC_66"
/clone_lib="Orary; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: Ovary; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_tib="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
/note="Vector: DR4-TOPO; Site 1 become as templates for
with_oligoribonucleotides and then used as templates for
                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3859127"
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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76.0%;
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Pred. No. 2e+03;
0; Mismatches 6;
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 35)
                                                                                                                                                                                                                                                                                                                          34 AMATCCGTTTGCTCAAAAAAAAAAAAAAAAAA 2
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Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Shrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 34)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                     CF310898 35 bp mRNA linear EST 15-AUG-2003 ABF--05-N05.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Cryza sativa cDNA clone ABF--05-N05, mRNA sequence.
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                                                                                                              Oryza sativa
                                                                                                                                                   CF310898.1
                                                                                                                                                                       CF310898
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="R.Goli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--02-M02"
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Pred. No. 2e+0
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Pred. No. 2e+03;
0; Mismatches
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                              Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
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Location/Qualifiers
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/clone lib*ABF3-overexpressing transgenic rice plasmid /clone lib*ABF3-overexpressing transgenic rice plasmid /cDNA lībrary (ABP)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
/tissue_type="callus"
/dev_stage="proliferated
/lab_host="E.coli DH10B"
                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/cultivar="Nackdong"
                                                               /db_xref="taxon:4530"
/clone="HD--01-p23"
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'clone="ABF--05-N05"
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                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
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                       callus
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                       for 2 weeks"
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DEFINITION

CF317946 20 bp mRNA linear solito-Avorexpressing transgenic rice plasmid cDNA

EST 15-AUG-2003

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VERSION
KEYWORDS
RESULT 1379
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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CF313752
CF313752.1 GI:33685513
EST.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for Ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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/mol_type="mRNA"
/cultivar="Nackdong"
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1 OsHDAC1-overexpressing transgenic rice plasmid cL
Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
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Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
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, MyongJi University
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CF339443
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Best Local Similarity
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                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                              1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                       Oryza sativa
Oryza sativa
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CF339443.1 GI:33827271
                                                                                                                                                                                                                                                                                                                                                                              CF339443 20 bp mRNA linear EST 18-AUG-2003 RCL1--04-003.gl Regenerated callus lambda phage cDNA library (RCL1) Cryza sativa cDNA clone RCL1--04-003, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
                                                                                                                  Contact: Nahm B.H.
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CF317946.1 GI:33689707
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bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--07-N06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="0HDAC1-overexpressing transgenic rice plasmid
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Pred. No. 1.2e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                         bhnahm@ggbio.com,
               /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; CDNA was inserted into lamda Uni-ZAP XR vector at end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs
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regenerated media"
                                                                                                                                                                                                                            /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/clone lib="Regenerated callus lambda phage cDNA library (RCL1)"
                                                                                                      /Glone lib="Regenerated callus lambda phage cDNA library
(RCL1)"
                                                                                                                                       tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="B.coli SOLR"
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/db_xref="taxon:4530"
/clone="RCL1--04-003"
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Pred. No. 1.2e
0; Mismatches
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Query Match Best Local S Matches 17

0.2%; 1 Similarity 85.0%; 17; Conservation

<u>,</u>

Score 15.2; DB 1 Pred. No. 1.2e+03 0; Mismatches

DB 1;

Length 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0080 row: K column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ345646 20 bp DNA linear GSS 29-SEP-20. IM0080K20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic importung UUGCIM0080K20 F, genomic survey sequence.
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Seq primer: CGTTGTAAAACGACGGCCAGT
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801 585 7177
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Laboratory Mouse DNA Resources (documents/dnares). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="UUGC1M0080K20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male
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Rodentia;
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RESULT 1383
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Noederhausern, and Wright,D.,Welss,R.
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GSS.
Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 20)
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Seq primer: CACACAGGAAACAGCTATGACC
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Insert Length: 10000 Std Err
Plate: 0192 row: N column: 1
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (2000)
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Fax: 801 585 7177
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                                                                                                                                               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pDM42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                           adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pw042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC1M0192N15"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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0.2%;
85.0%;
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  Score 15.2; DB 1;
Pred. No. 1.2e+03;
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AZ592714
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5781 TGCCTGCCTGCCTGCC 5800
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High quality sequence stop: 20.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0403 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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1M0403P13R Mouse 10kb plasmid clone UUGC1M0403P13 R, genomic
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                                                        Conservative
                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       whole genome scaffolding with paired end reads from 10kb
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strain="C57BL/6J"
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                                                                                                              Score 15.2; DB 1; Length 20; Pred. No. 1.2e+03;
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                                                                                        Mismatches
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                                                                                  Gaps
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VERSION
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IM0466E16R Mouse 10kb plasmid UUGC1M library Mu
clone UUGC1M0466E16 R, genomic survey sequence.
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Location/Qualifiers
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Insert Length: 10000 Std Error: (
Plate: 0466 row: E column: 16
Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B.
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Fax: 801 585 7177
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                                                                                                 Conservative
                                                                                                                                                                                                           /clone lib="Mouse 10kb plasmid UUGCIM library"
/notee"Vector: pWD42TV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-GOld (Stratagene) cells
and selected for ampicalling resistance "
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/strain="C57BL/6J"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Insert Length: 1000 Std Error:
Plate: 0282 row: O column: 04
Seq primer: CGTTCTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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21 bp DNA line
1M0282004F Mouse 10kb plasmid UUGC1M library Mu
clone UUGC1M0282004 F, genomic survey sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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801 585 7177
                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                              adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Location/Qualifiers
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Insert Length: 1000 Std Error:
Plate: 0465 row: C column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GSS.
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                  Conservative
                                                                                                                                                                                             Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                          Pred. No. 1...
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                                                                                                                          Score 15.2; DB 1;
Pred. No. 1.3e+03;
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UUGC1M library Mus musculus genomic
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                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb
Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                AZ854229
22 bp DNA linear GSS 2: 2M0157C14R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0157C14 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                        AZ854229
AZ854229.1 GI:13043139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS.
                                                                Unpublished (2000)
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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AL454378
AL454378.1 GI:11855182
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/strain="TREU927"
/db_xref="taxon:5691"
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Pred. No. 1.3e+03;
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Nouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ470212 22 bp DNA linear GSS 04-OCT-200
1M0284L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0284L09 F, genomic survey sequence.
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GSS.
Mus musculus (house mouse)
University of Utah Genome Center University of Utah
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Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: C column: 14
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Tel: 801 58
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 22)
1 (Dases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ875902 22 bp DNA linear GSS 21
2M0190K12R Mouse 10kb plasmid UUGC1M library Mus musculus
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Insert Length: 10000 Std Error: 0.00
                                                                                 Unpublished (2000)
Contact: Robert B.
                                                                                                                                  plasmid inserts
                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ875902.1 GI:13086357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone UUGC2M0190K12 R, genomic survey sequence.
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwp42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0284L09"
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Pred. No. 1.4e+03;
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hes 3;
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AL587602/c
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Best Local Similarity
Matches 17; Conserv
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Insert Length: 10000 Std Error: (
Plate: 0190 row: K column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                AL587602.1 GI:13192636
EST.
Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                            Roslin Institute
Roslin, Midlothian, EH25
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                 Unpublished (2001)
Contact: Frazer Murray
                                                                                                                                                                                                           Murray, F.
BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL587602 BP Chicken Brain Library
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Fax: 801 585 7177
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTTTT 3' Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROS059F08, mRNA sequence.
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                                                                                                                                        Genomics and Bioinformatics
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
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/strain="C57BL/6J"
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mol_type="qenomic מאם"
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Pred. No. 1.4e+03;
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  Poly A RNA purchased from Clonetech
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AZ308643
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Best Local Similarity
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Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: 0 column: 13
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (2000)
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome
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                                                                                                                                                                                                                                                                  quality sequence stop: 23.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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clone="UUGC1M0011013"
                                                                                                                                                                     organism="Mus musculus"

(mol_type="genomic DNA"

(strain="C57BL/6J"
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/db_xref="taxon:9031"
                                                                                                                    sex="Male"
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Pred. No. 1.5e+03;
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SOURCE
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AZ345908/c
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ345908 23 bp DNA linear GSS 29 100080F22R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0080F22 R, genomic survey sequence.
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse_10kb_plasmid_UUGCIM_library" /note="Vector: PWD42nv." purified_genomic_DNA_from nusculus_CSTBL/60_(male) was obtained_from the_Jac_Laboratory_Mouse_DNA_Resource_(http://www.jax.org/resources/documents/dnares/). 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical
                                                                                                                                                                                                   /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                            clone="UUGC1M0080F22"
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Pred. No. 1.5e+03;
0; Mismatches 3;
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was hydrodynamically sheared by repeated passage through

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AZ468097
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rockes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plagmid incorts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 23)
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1M0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0279K22 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 10000 Std Error: 0.00 Plate: 0279 row: K column: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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USA
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                                                                      Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0279K22"
                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                 'sex="Male"
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Pred. No. 1.5e+03;
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AZ970753
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2M0244E01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0244E01 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 01
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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AZ970753.1 GI:13841980
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                                                                                                /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jack.
Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
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was blunt end-repaired with T4 DNA polymerase and
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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AZ437459/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.; Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ437459 26 bp DNA linear GSS 03-OCT-200
1M0225B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone.UUGC1M0225B15 R, genomic survey sequence.
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17; Conserv
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Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were
                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pW042nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                 sex="Male
                                                                                                                                                                                                                                                                                                       clone="UUGC1M0225B15"
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                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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DEFINITION RESULT 1399 TA327D04P/c

TA327D04P
T. brucei sheared genomic DNA genomic survey sequence.

bp DNA :

linear forward

sequence, GSS 13-DEC-2000

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REFERENCE
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Best Local Similarity
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Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW332443 28 bp mRNA linear EST S8E7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: staben@pop.uky.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 606 257 2161 Fax: 606 257 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          School of Biological Sciences University of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Staben C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW332443.1 GI:6828800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 Morgan Building, University of Kentucky, Lexington, KY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pneumocystidaceae; Pneumocystis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWHA2 (gi.4732114 gb.AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                       Conservative
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                                                                                                                                                                         /clone lib="AGS-1"
/clone lib="AGS-1"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (59-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene, Further
details see www.uky.edu/Project/Pneumocystis/"
                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db xref="taxon:4754"
/lab host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Pneumocystis carinii"
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Pred. No. 1.8e+03;
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                                                                                       8
                                                                                                                               Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrell, Oxford Universary .......
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                        1 (bases 1 to 29)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF314795 29 bp mRNA linear EST 15-AUG-HD--03-H09.gl OsHDAC1-overexpressing transgenic rice plasmid cDlibrary (HD) Oryza sativa cDNA clone HD--03-H09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hir Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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Oryza sativa
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GSS.
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1 (bases 1 to 28)
                                                                 Email: bhnahm@ggbio.com,
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/organism="Oryza sativa"
                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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Pred. No. 1.9e+03;
                                                                 bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ586486 29 bp mRNA linear EST (
E012391-024-012-J22-SP6 MPIZ-ADIS-024-leaf Beta vulgaris
024-012-J22 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 12 row: J column: 22
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22362189
12472698
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Construction of a 'unigene' cDNA clone set by oligonucleotide Construction allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
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1 (bases 1 to 29)
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Beta vulgaris
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BQ586486.1 GI:26116068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lei
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                                      /clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone lib="OsHDAC1-overexpressing transgenic rice placeDNA library (HD)"
CDNA library (HD)"
/note="Vector: pcR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derived from rice Histone Deacetylase overexpression
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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/cultivar="Nackdong
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
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/clone="HD--03-H09"
                                                                                                                                                                                                                                                                                                       /mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                 tissue_type="leaf"
                                                                                                                                                                                                            'db_xref="taxon:161934"
'clone="024-012-J22"
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                                                                                                                                                                                                                                                                                                                                                organism="Beta vulgaris"
                                                                                                                                                              lab_host="EMDH10B"
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Pred. No. 2e+03;
0; Mismatches
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                                                                                                                                                                                                                       4015 ATGAGAAAAAGAGAGAAAACAAAATGT 4042
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T. brucei sheared genomic genomic survey sequence. AL497621
AL497621.1 GI:11873343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Unpublished (2003)
                                                                                 TA378G07P
                                                                                                                                                                                                                                                               h 0.2%;
Similarity 71.4%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                           /dev_stage="14 days after germination"
/lab host="E.coll DH10B"
/clone lib"ABF3-overexpressing transgenic rice plasmid
/clone lib"ABF3-overexpressing transgenic rice plasmid
/cDNA lībrary (ABF)"
/note="Vector: pCR4-TOP0; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultivar="Nackdong"
db_xref="taxon:4530"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="leaf"
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                                                            GSS 13-DEC-2000 sequence,
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Best Local
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                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3271 TTTGTTTAAGAAGAAAATGAAACCAGA 3298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                              Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF336137

29 bp mRNA linear EST 18-AUG-20 JMT--06-B10.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza Bativa cDNA clone JMT--06-B10, mRNA sequence. CF336137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to give a tight size distribution ( 4\ kb ). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith, H. and Venter, J.C. (Making smalescribed in detail in Smith)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                   Yongin, Kyeonggi, K
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of T. brucei sequencing at the Sanger at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF336137.1 GI:33820654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall, N., Bowman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%;
Similarity 71.4%;
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                                                                                                                        bhnahm@ggbio.com, bhna
Location/Qualifiers
organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="378g07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/strain="TREU927"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.2; DB 1;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                            bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shin, Y.C.
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RESULT 1405
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Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0230 row: I column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ962183 30 bp DNA linear GSS 27-APR-200
2M0230I24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0230I24 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
High quality sequence stop: 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20
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/lab_host="5.coll DH108"
/clone lib="AtJWT-overexpressing transgenic rice plasmid
/clone Library (JWT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                             /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methyltransferase overexpression line."
                                                                                                                                                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0230I24"
                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="leaf"
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                                                                                                                                                                                                                                                                                           sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus'
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COMMENT

JOURNAL

TITLE

FEATURES

밁 8 VERSION KEYWORDS

ACCESSION

REFERENCE

AUTHORS

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Matches

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ACCESSION
VERSION
KEYWORDS
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SOURCE
ORGANISM
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VERSION
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DEFINITION
                                                                                                                        RESULT 1407
BG501238
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AU268044
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 SOURCE
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                                                                                                                                                                                                                 4012 АЛАЛТGАGAAAAAGAGAGAAAACAAAA 4039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4014 AATGAGAAAAAAGAGAGAAAACAAAATG 4041
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                                                   mRNA sequence.
BG501238
                                                                                 BG501238
602547802F1 NIH_MGC_60 Homo
                                                                                                                                                                                                2 AAAACAAAAAAAAAAATTAAAAAAAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular stages of Dictyostellum discoideum
Unpublished (2002)
                BG501238.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 31)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-298-53-4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-1-1 Tennoudai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hideko Urushihara
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sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwh2 (gi| 4732114| gb| AFT29072.1), a copy-number inducible derivative of plasmid kl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostelium
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                   /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="VSH836"
                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                            sex="mat A"
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Pred. No. 2e+03;
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AW250841/c
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                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information
be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                              Unpublished (1999)
Other_ESTs: 2821274.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                   AW250841.1 GI:6593834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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Tissue Procurement: DCTD/DTP
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1 (Dases 1 to 32)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCAAAAAAAAAAAAAAAAAAAAAAA 32
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3' -ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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Site 1: Sfil (ggccgcctcggcc); Site 2: Sfil
(ggccattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
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/mol type="mRN0"
/db xref="taxon:9606"
/clone="IMAGE:4670136"
/clone="IMAGE:4670136"
/tissue_type="adenocarcinoma"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
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sapiens cDNA clone IMAGE:2821274 3',
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CF279813/c
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Infiliation, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF279813 32 bp mRNA linear EST 14-AUG-20
14ETL--06-E02.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--06-E02, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Plate: LLCM6 1
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Location/Qualifiers
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/lab Nost="DH108 (phage-resistant)"
/lab Nost="DH108 (phage-resistant)"
/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                           bhnahm@ggbio.com, bhnahmannahm@gbio.com, bhnahmannahm@gbio.com, bhnahmannahm@gbio.com, bhnahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmannahmann
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                 organism="Oryza sativa"
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/mol_type="mRNA"

/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
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                                4020 AAAAAAGAGAGAAAACAAAATGTTATTT 4047
32
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                        Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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Genome Biol. 4 (10), R63
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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                                                                      Conservative
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                                                                                                                                                                                                                                                                        organism="Glossina morsitans morsitans"
|mol_type="mRNA"
|sub_species="morsitans"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
                                                                                                                                                                                               /clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                    /clone="Tse36f08_p1c"
/tissue_type="adult infected gut"
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Pred. No. 2.1e+03;
0; Mismatches 8
                                                                   Score 15.2; DB 1;
Pred. No. 2.1e+03;
0; Mismatches B
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        Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 32)
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morsitans morsitans cDNA clone Tse50g08_plc, mRNA sequence.
                                                                                                                                                                                             BX564047 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse6d04_plc, mRNA sequence.
                                                                                                                    Glossina morsitans morsitans
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Tse50g08_p1c"
/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Glossina morsitans
/mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="country: Zimbabwe;
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Aksoy, S., Gibson, W., Kerhornou, A.,
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University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are
end of the CDNA all plc reads,
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                    Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 3)
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            University of Wales,
Bangor LL57 2UW
All clones with suff:
                                                                Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                             Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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Genome Biol. 4 (10), R63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Tse6d04 plc"
/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected gut"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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Pred. No. 2.1e+03;
0; Mismatches 8
            qic are
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            reverse
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          primer reads starting at
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BE230585/c
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                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. a
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Spermatodeae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis of ESTs from Rice Seedling Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE230585 15 bp mRNA linear EST 07-JI
99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
(indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end of the cDNA all plc reads
the 3' end.
Location/Qualifiers
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e,M.C., Shin,Y.C.,
                                                                     Conservative
                                  TTTTTTTTTT 4478
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                                                                                                                                                                                                                                                                                                                                                                                      myeun@sun20.asti.re.kr
                                                                                                                                        /dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site"
                                                                                                                                                                                                                                                      /organism="Oryza sativa (indica cultivar-group)"
|mol type="mRNA"
|cultivar="Milyang23"
|/db xref="taxon:39946"
|/clone="99A5799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.brucei"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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                                                                                        Score 15;
Pred. No.
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                                                                                                       DB 1;
                                                                                      6.9e+02;
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8
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RESULT 1415

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                                                                                                                                                                                                                                                                                                                   4464 TT
Beta vulgaris
Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                 15 bp mRNA linear EST 06-DEC-2002
E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-014-H17 5-PRIME, mRNA sequence.
EQ585820
EQ585820.1 GI:26115402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)
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Length: 15 Std Brror: 0.00
7 row: B column: 02
imer: T7; GTAATACGACTCACTATAGGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clome lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not!;
/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not!, primer sites and
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/clone="024-007-B02"
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/mol_type="mRNA"
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BQ590410
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                                                                                       and Radelof, U.
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4464 TTTTTTTTTTTTTT 4478
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet grant J. 32 (5), 845-857 (2002)
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BQ590410.1 GI:26119993
EST.
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Plate: 14 row: H column: 17
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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                                                                                                                                                                                                    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lef
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/lab_host="MDH108"
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/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Notl;
/note="Vector: pcMVSPORT6; Set 1: Ibrary provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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CONTACT: Weisshaar B
ADIS DNA core facility at MPIZ
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BQ590656.1 GI:26120239
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Email: weisshaa@mpiz-koeln.mpg.de
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Carl-von-Linne Weg 10, 50829 Koeln,
Fax: 00492215062851
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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/lab_host="EMDH10B"
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ADIS DNA core facility at MPIZ
Max-planck-Institute for Plant Breeding Research
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                                                                                                                                                                                                                Email: weisshaa@mpiz-koeln.mpg.de
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
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/note="Vector: pCMVSPORT6; Site 1: Salt; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
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/db_xref="taxon:161934"
/clone="024-017-N18"
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/mol_type="mRNA"
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                                                                                                                                                                                         location/Qualifiers
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/mol_type≈"mRNA"
                                                                                                cultivar="KWS2320 (double haploid, monogerm breeding
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/lab_host="EMDH10B"
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100.0%; Pred. No. 6.9e+0
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4464 TTTTTTTTTTTTTT 4478
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1 (bases 1 to 15)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet grant J. 32 (5), 845-857 (2002)
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BQ591178.1 GI:26120761
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ert Length: 15 Std Error: 0.00
te: 17 row: F column: 22
primer: T7; GTAATACGACTCACTATAGGGC
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordin
                                                                                           /clome lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Salt. Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Salt. Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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/note="Vector: pcMvSPORT6; Site 1: Salte 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                                                                             orientation:
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/lab_host="EMDH10B"
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/clone="024-017-F22"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Beta vulgaris"
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00.0%; Pred. No.
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Menze,A., O'Brien,J., Lehrach,H
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    coordinator:
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Matches Query Match Best Local

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SOURCE KEYWORDS

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AUTHORS

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Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
100.0%;
                     0.2%;
     Score 15;
Pred. No.
                     DB 1;
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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Beta vulgaris
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E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA Clone 024-017-H02 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carl-von-Linne Weg 10, 50829 Koeln,
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                                                                                                                 Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                          /clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORTS; Site 1: Salt; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
cDNA library from sugar beet, library Germany, contact
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
                                                                                         RZPD/GABI-Primary database: http://gabi.rzpd.de"
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lab_host="EMDH108"
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/db_xref="taxon:161934"
/clone="024-017-H02"
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/mol_type="mRNA"
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  0.2%;
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  Score 15;
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AUTHORS
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Matches 15; Conserv
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CF277319

15 bp mRNA linear EST 14-AUG-2003
14ETL--02-M23.bl Rice etiolated leaf plasmid cDNA library (14ETL)
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Insert Length: 15 Std Error: 0.00
Plate: 24 row: M column: 05
Seg primer: T7; GTAATACGACTCACTATAGGGC.
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ADIS DNA core facility at MPIZ
AMAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ594689 15 bp mRNA linear E E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root CDNA Clone 024-024-M05 3-PRIME, mRNA sequence.
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Email: weisshaa@mpi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="MPIZ-ADIS-024-developing root"
/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="developing root"
/lab_host="EMDH10B"
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/clone="024-024-M05"
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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100.0%; Pred. No. 6.9e+0
live 0; Mismatches
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hes 0;
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CF281923
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Oryza sativa
Oryza sativa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Entharyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzaa;
Oryza.

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                    Yongin, Kyeonggi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                         1 (Dases 1 to 15)
1 (Dases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                      Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence. CF281923
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Pax: 82 31 321 6355
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Location/Qualifiers
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/mol type="mRNA"
/culTivar="Nackdong"
/culTivar="Nackdong"
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/db_xref="taxon:4530"
                                                                                  organism="Oryza sativa"
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3. 6.9e+02;
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CF291029
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Best Local
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15; Conserva
                                                                                                                                                                                   15;
CF291029 15 bp mRNA linear EST 14-AUG-14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Song,S.I., Sim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Unpublished (2003)
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Wackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-C09"
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/lab host="E.coli DH10B"
                                                                                                                                                                                                                                                /clone lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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with oligoribonucleotides
RT-pCR."
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(14ETL)
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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Pred. No.
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CF291103
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Best Local
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1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF291103 15 bp mRNA linear EST 14-AUG-14ROOT--01-G10.bl Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-G10, mRNA sequence.
                                                                                  Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF291029.1 GI:33660062
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/clone="14ROOT--01-E19"
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/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/lab host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mENA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
/organism="Oryza sativa"
/mol_type="mRNA"
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Pred. No. 6.9e+02;
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                                                                                                                  bhnahm@bio.myongji.ac.kr
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RESULT 1429
CF291798
LOCUS CF291798 15 bp mRNA linear EST 14-AUG-2003 DEFINITION 14ROOT--02-G02.bl Rice root plasmid cDNA library (14ROOT) Oryza
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CF291717
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Best Local Similarity
Matches 15; Conserv
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Best Local (
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa
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CF291717.1 GI:33660750
EST.
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15 bp mRNA linear EST 14-AUG-2003
14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-E04, mRNA sequence.
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                                                                                                                                                                                                                                      0.2%; Score 15; DB 1; Locality 100.0%; Pred. No. 6.9e+02; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mrNA"
/mol_type="mrNA"
/mol_type="mrNA"
/culTiva="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli DHIOB"
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/clone_Tib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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/clone="14ROOT--01-G10"
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100.0%; Pred. No. 6.9e+02;
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VERSION
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CF292458
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                               1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                 Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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    Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
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CF291798
CF291798.1 GI:33660831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
               Location/Qualifiers
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15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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 CF296652
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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/lab_host="E.coli DH10B"
/clome_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-G17, mRNA sequence.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Oryza sativa
                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="Nackdong"
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
bhnahm@ggbio.com, bhn
Location/Qualifiers
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Pred. No. 6.9e+02;
                                                       bhnahm@bio.myongji.ac.kr
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7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--02-B23, mRNA sequence.
CF298630
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15; Conserv
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/clone="7LEAF--02-B23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/ab_host="E_coli bH108"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
RT-PCR."
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/lab host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_Tib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with_oligoribonucleotides and then used as templates for
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/clone="7LEAF--01-G17"
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 6.9e+02;
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Best Local 9
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                  Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                               Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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7LEAF--02-G20.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-G20, mRNA sequence.
                                       Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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    Location/Qualifiers
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82 31 321 6355
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bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/lab host="E.coli DHIOB"
/clome_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clome_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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100.0%; Pred. No. 6.9e+02;
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(7LEAF) Oryza
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Fax: 82 31 321 6355
μ.
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Genomics and Genetics Institute, Greendene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kyeonggi, Korea
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with oligoribonucleotides and then used as templates for
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/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                   100.0%;
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100.0%; Pred. No.
                                                                                                   0.2%;
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                                                                                   Score 15;
Pred. No.
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                                                                               DB 1; Le
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AUTHORS
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CF299608
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RESULT 1438

bhnahm@ggbio.com,

bhnahm@bio.myongji.ac.kr.

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Query Match 0.2%;
Best Local Similarity 100.0%;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 bp mRNA linear 7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--03-L04, mRNA sequence. CF299608
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                              Oryza sativa
Guraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF299608.1 GI:33671369
                                                                                                                                              Contact: Nahm B.H.
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with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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; Pred. No. 6.9e+02;
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(7LEAF) Oryza
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                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local (
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7LEAF--04-G12.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA cione 7LEAF--04-G12, mRNA sequence.
CF300121
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University
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EST.
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                   Conservative
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Location/Qualifiers
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                                                                                                                                      0.2%;
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                                                                                                             Score 15; DB 1; L
Pred. No. 6.9e+02;
0; Mismatches 0;
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                                                                                                                                                                 Length 15;
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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CF300992
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CF300361
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Best Local Sim
Matches 15;
                                                                                                             TITLE
JOURNAL
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JOURNAL
                                                                                                                                                                                                AUTHORS
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Oryza sativa
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4464 TITTTTTTTTTTT 4478
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 15)
1 (bases 1 to 15)
1 (bases 1, Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidaae; Oryzeae; Oryza.
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Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Fax: 82 31 321 6355
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7LEAF--04-L16.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-L16, mRNA sequence.
CF300361
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    Location/Qualifiers
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 6.9e+02;
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(7LEAF) Oryza
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CF302034
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Feax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
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                                                                                                   0.2%; Score 15; DB llarity 100.0%; Pred. No. 6. Conservative 0; Mismatches
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                                                                                                                                                                                               /organism="Oryza sativa"
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/mol_type="mRNA"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="PLEAF-07-024"
/tissue_type="leaf"
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/lab_host="E.coli_DH10B"
/clone_"lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Location/Qualifiers
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/db_xref="taxon:4530"
/clone="7LEAF--05-K19"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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                                                                                             DB 1; 5.
5. 6.9e+02;
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(7LEAF) Oryza
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CF302182
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Best Local Similarity
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CF302182
CF302182
CF302182.1 GI:33673943
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                                                                                                                                                                                      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs (npublished (2003)
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7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
CF302124
                                                                                               1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
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Yongin, Kyeonggi, k
Tel: 82 31 330 6193
                                                                                  Contact: Nahm B.H.
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Location/Qualifiers
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/note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was cappe
with oligoribonucleotides and then used as templates for
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|mol_type="mRNA"
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DEFINITION
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CF307923
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University YongIn, Kyeonggi, Korea
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Email:
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                                                           /cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--01-I15"
/tissue_type="leaf"
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="texcon:4530"
/clone="7LEAF--07-H20"
/tissue_type="leaf"
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/clone lib="RE.coli DH108"
/clone lib="RE.col overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
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                                        0.2%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 6.9e+02;
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                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            bhnahm@bio.myongji.ac.kr
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                       AUTHORS
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1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                            Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                          CF311907 15 bp mRNA linear EST 15-AUG-2003 ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence. CF311907
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
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Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF311159
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA lībrary (ABF)"
cDNA lībrary (ABF)"
/note="vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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100.0%; Pred. No. 6.9e+02;
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RESULT 1449
CF313319
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AUTHORS
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                        Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF313319.1 GI:33685080
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Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                    bhnahm@ggbio.com, bhnahm@bio.
                                                                                                    /organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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/clone="ABF--07-G04"
'dev_stāge="proliferated callus on 2N6 media for 2 weeks"
'lab_host="E.coli DH10B"
'Calome lib="OSHDAC1-overexpressing transgenic rice plasmic
DNA lībrary (HD)"
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mol_type="mRNA"
                                                                                   tissue_type="callus"
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RESULT 1451
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CF313320/c
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Gryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrharcoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
               HD--05-H15.b1 OsHDAC1-overexpressing transgenic rice plasmid cllibrary (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.
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15; Conserv
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Tel: 82
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82 31 330 6193
82 31 321 6355
                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                           derived from rice Histone Deacetylase overexpression line." % \begin{array}{ll} & & & & \\ & & & \\ & & & \\ & & & \\ \end{array} \label{eq:continuous}
                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="proliferated callus on 2N6 media for 2 weeks"
lab_host="B.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="HD--01-G13"
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                                                                                                                                                                                                                                                 100.0%;
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Pred. No.
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Pred. No. 6.9e+02;
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SOURCE
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CF318035
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          Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbbo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               HD--07-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence. CF318035
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                            Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli_DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No.
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CF327434
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Query Match
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
Oukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NACL--01-018.bl Rice callus plasmid con library (NACL) sativa cDNA clone NACL--01-018, mRNA sequence.
CF327434
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                          /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 c
/dev_stage="proliferated callus on 2N6 media for 30 c
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was cap
with oligoribonucleotides and then used as templates
RT-PCR."
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--07-P06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/Clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pCR4-TOPO; Site_1: ECORI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                             /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="NACL--01-018"
0.2%;
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Score 15;
Pred. No.
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DB 1; Lo
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6.9e+02;
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CF330195
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Best Local Similarity
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                                                                                                                                                                                                         Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
                                                                                                     1 (bases 1 to 15)

Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                   CF330668 15 bp mRNA linear NACL--06-H16.b1 Rice callus plasmid cDNA library sativa cDNA clone NACL--06-H16, mRNA sequence.
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CF330668.1
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/clone="NACL--05-N03"
/tissue_type="callus"
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CF332178
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Best Local Similarity
Matches 15; Conserv
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CF332178
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Song,S.I., Kim,J.K., Kim,Y.-K. and
Large-scale Sequencing Analysis of
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Oryza sativa
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Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   gin, Kyeonggi, Ko
82 31 330 6193
82 31 321 6355
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                                       Conservative
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|mol type="mRNA"
|cultivar="Nackdong"
|/db xref="taxon:4530"
|/clone="NACL--06-H16"
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/note="Vector: pCR4-TOPO;
with oligoribonucleotides
RT-PCR."
                                                                                                                        /clone lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                      /clone="NACL--08-J10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days" .
/lab_host="E_coli_DH10B"
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| Jab_host="B_coli DH10B"
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db_xref="taxon:4530"
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|mol_type="mRNA"
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ligoribonucleotides and then used as templates
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Pred. No.
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                                                     DB 1; L, 6.9e+02;
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CF336202
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                                                                 TITLE
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and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                    BQ590507 16 bp mRNA linear EST 06-DEC-:
E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
BQ590507
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Contact: Nahm B.H.
                                                                                                  Eukaryotā; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (Dases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                           Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
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MT--06-C20.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
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Oryza sativa
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EST.
                                                                                                                                                                                                                                                                       Beta vulgaris
                                                                                                                                                                                                                                                                                                                 BQ590507.1 GI:26120090
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="leaf"
/dev stage="14 days after germination"
/lab host="E.Coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methyltransferase overexpression line."
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--06-C20"
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100.0%; Pred. No.
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BQ595369
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PUBMED
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Best Local
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                                                            Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                    Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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16 bp mRNA linear EST 06-DEC-200: S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris CDNA clone 024-022-P02 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                        Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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[ (bases 1 to 16)
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Beta vulgaris
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12472698
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02
                                                                                                                                                                                                                     22362189
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Insert Length: 16 Std Error: 0.00
Plate: 19 row: M column: 04
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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ADIS DNA core facility at MPIZ
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/note="Vector: pcMVSPORT6; Site 1: Salt, Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               orientation:
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/lab_host="EMDH10B"
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/clone="024-019-M04"
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/mol_type="mRNA"
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1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Large-scale Sequencing Analysis 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
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/note="Vector: pcMVSPORT6; Site 1: Sal1; Site 2: Not1;
/nota="Vector: pcMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, llbrary provided by KWS
Clainwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
/cullivar="Nackdong"
/db xref="taxon:4530"
/db xref="taxon:4530"
/clone="30DGS--06-F22"
/tissue_type="leaf"
/dev stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice|leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capp
with oligoribonucleotides and then used as templates f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.dem
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/lab_host="EMDH10B"
                                                                                                                                                                                                                    organism="Oryza sativa"
|mol_type="mRNA"
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|mol_type="mRNA"
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; Pred. No.
                                                                                                                                                                                                                                                                                                                  bhnahm@bio.myongji.ac.kr
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              capped
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CF314013
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CF329320
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Best Local
                                                                              ORGANISM
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Best Local
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                16 pp mRNA linear EST 18-AU
NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-J17, mRNA sequence.
CF329320
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                                                                                                                                                 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bhnahm@ggbio.com, bhnahm@gbio.com, bhnahm@ggbio.com, bhnahm@gbio.com, bhnahm@gbio.co
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="HD--02-G01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E_coli_DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No.
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Pred. No.
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8e+02;
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CF311499
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Best Local Similarity
Matches 15; Conserv
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)

2 (bases 1 to 17)

3 (bases 1 to 17)

3 (bases 1 to 17)

4 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@ggbio.com,
                                                                                                                                        /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF--06-L20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                          /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4530"
/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media
/lab_host="E.coli DH10B"
clone_lib="ABF3-overexpressing transgenic
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB; Pred. No. 8e+
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                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@bio.myongji.ac.kr
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CF301359 18 bp mRNA linear 7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--06-D05, mRNA sequence. CF301359 CF301359.1 GI:33673120 EST.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1 (Dases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
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15; Conservative
                                                                                                                                                                                                 TTTTTTTTTTTTT 4478
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--02-A20"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                     /dev_stage="7 days after germination"
/lab host="E.coli DHIOB"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notc="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was cappe
with oligoribonucleotides and then used as templates fo
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3. 9.1e+02;
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                                                                     EST 15-AUG-2003
(7LEAF) Oryza
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ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                     of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.

Song,S.I., Xim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Similarity 100.0%; Pred. No. 1e+03;
15; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
                                                                                                                                                bhnahm@ggbio.com,
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/clone="7LEAF--06-D05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="8.coli DHIOB"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
/note="Vector: pCR4-TOPO; Site_1: Book as templates for
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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                                                                                                                                                bhnahm@bio.myongji.ac.kr
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Best Local Similarity 100.0%;
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CF329485 18 bp mRNA linear EST 18-AUG-2003 NACL--04-N06.gl Rice callus plasmid cDNA library (NACL) Oryza
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF329484.1 GI:33807207
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/mol_type="mRNA"
/mol_type="mRNA"
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/clone="NACL--04-N06"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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/lab_host="E.coli DH10B"
/clome lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1; Length 18; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bhnahm@bio.myongji.ac.kr
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Best Local Similarity
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                              Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                    Contact: Nahm B.H.
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CF329485
CF329485.1 GI:33807209
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                                        bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="NACL--04-N06"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RT-PCR."
/organism="Oryza sativa"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E_coli DH10B"
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Pred. No. 1e+03;
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    15;
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.;

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrharroideae; Oryzae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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19 bp mRNA linear EST 15-AUG-2003
ABF--01-L07.bl ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--01-L07, mRNA sequence.
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CF308042.1 GI:33679803
                      Similarity
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Similarity 100.0%;
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Location/Qualifiers
                                                                                 element
line."
                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/cultivar="Nackdong"
/cultivar="taxon:4530"
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                                                                                           /tissue_type="leaf"
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/lab_host="E.coli DH108"
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cDNA lībrary (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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with oligoribonuclectides and then used as templates for
RT-DOP "
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/dev_stage="14 days after germination"
/lab_host="8.coli DH10B"
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                                                                                                                     Local Similarity
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Insert Length: 10000 Std Error:
Plate: 0276 row: E column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from
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Unpublished (2000)
Contact: Robert B.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Mammalia; Eutheria; Rodentia;
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801 585 7177
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Location/Qualifiers
                                                                                                Conservative
                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH2 (gi |4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male"
                                                                                                                     100.0%;
                                                                                                                     0.2%; Score 15; DB 1; Lo
100.0%; Pred. No. 1.1e+03;
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UUGC1M library Mus musculus genomic
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AZ596349
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                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse, whole genome scaffolding with paired end reads from 10kb
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 bp mRNA linear EST 14-AUG-20 14ETL--09-I22.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--09-I22, mRNA sequence.
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University of Utah University of Utah
                                         Contact: Robert B.
                                                         Unpublished
                                                                              plasmid inserts
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ETL--09-I22"
/tissue_type="leaf"
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| dab_host="E.coli DH10B"
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Pred. No.
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1.3e+03;
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                                                                                                                 JOURNAL
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                     Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1M0128E13R Mouse 10kb plasmid clone UUGC1M0128E13 R, genomic
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Location/Qualifiers
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Insert Length: 10000 Std Error: (
Plate: 0409 row: K column: 03
Seq primer: CACACAGGAAACAGCTATGACC
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Tel: 801 585 5606
Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
muscullus CS7BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW942 (gi | 4732114 | gb | AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli xilo-Gold (Stratagene) cells
and selected for amnicillin resistance "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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100.0%; Pred. No. 1.4e+03;
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                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ425710 23 bp DNA linear GSS 03-OCT-200 1M0205L23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0205L23 R, genomic survey sequence.
University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                           Contact: Robert B.
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High quality sequence stop: 22.
Location/Qualifiers
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Plate: 0128 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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  Biomedical Polymers Research Bldg.,
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/strain="C57BL/6J"
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                                           Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
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Seg primer: CACACAGGAAACAGCTATGACC
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Insert Length: 10000 Std Error: 0.00
Plate: 0205 row: L column: 23
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/clone="UUGC1M0205L23"
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strain="C57BL/6J"
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pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ817623 23 bp DNA linear GSS 20-FEB-200 2M0087N09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0087N09 F, genomic survey sequence.
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Location/Qualifiers
                                                                    University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
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78.3%;
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Pred. No. 1.6e+03;
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REFERENCE
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ORGANISM
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CF297907/c
                                                                           FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF297907 23 bp mRNA linear 7LEAF--01-B05.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--01-B05, mRNA sequence.
                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 23.
                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
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Plate: 0087 row: N
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Insert Length: 10000 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAAAAAAAAAAATTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                    bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
l. .23
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus C57BL/6J (male) was obtained from the Jackson
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Pred. No. 1.6e+03;
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(7LEAF) Oryza
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SOURCE
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BX560037
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  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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MEDLINE
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                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4012 AAAATGAGAAAAAAAGAGAGAAAA 4034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans
Glossina morsitans morsitans
Rukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.
                                                                                                                                                                                                                                                                                                                                   University of Wales,
Bangor LL57 2UM
All clones with suffix qlc are reverse
end of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EX560037 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans morsitans morsitans morsitans morsitans cDNA clone Tse47e08_plc, mRNA sequence.

EX560037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14519198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. 4 (10), R63 (2003) 22881942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hippoboscoidea; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX560037.1 GI:33368052
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  Conservative
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(cultivar="Nackdong"

(./db_xref="taxon:4530"

/clone="7LEAF--01-B05"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                        /clone="Tse47e08 plc"
/tissue type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected gut"
                                                                                    /note="country: Zimbabwe; EST from adult gut
T.brucei"
                                                                                                                                                                                                                              /mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                                                                                                     organism="Glossina morsitans morsitans"
                                                                                                                                                                                                                                                                                                                location/Qualifiers
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                     0.2%;
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Pred. No.
Score 15; DB 1;
Pred. No. 1.6e+03;
0; Mismatches '5
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                                           Length 23
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  0,
                                                                                                       infected with
  Gaps
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SOURCE
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AZ303987/c
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CB305256
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Best Local Similarity 78.3%;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                     23 bp DNA linear GSS 29-SEP-200
1M0003H22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0003H22 R, genomic survey sequence
AZ303987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: swangl@midway.uchicago.edu
This EST was detected from Drosophila melanogaster cDNA Library
With GLGI technique (Generation of Longer cDNA fragments from SAGI
tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349,
2000; A high-throughput GLGI procedure for converting a large
number of SAGE tag sequences into 3' ESTs, Genes, Chromosomes &
Cancers 33:252-261, 2002), which covers from the 3' end of cDNA
till the first CATG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB305256 23 bp mRNA linear 3'EST-Nfly-071 Drosophila melanogaster cDNA Library
                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 23)
                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Chicago Medical Center 5841 S. Maryland Ave., MC2115, Chicag Tel: 773-702-6788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila genome 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee,S., Zhou,G., Bao,J., Shapiro,J., Xu,J., Sun,M., Lin,W., Zhang,R., Chen,J., Clark,T., Sun,M., Wang,J., Johnson,D., Tseng,C., Yang,H., Wang,J., Du,W., Wu,C.I., Zhang,X. and Wang,S.M. Novel SAGE tags represent a significant number of novel genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                          AZ303987.1 GI:10339507
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/mol_type="mRNA;
/mol_type="mRNA;
/db xref="taxon:7227"
/clone_lib="Drosophila melanogaster cDNA Library"
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                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus
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AZ380872
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Nouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                AZ38087
                                                                                                                                                                                                                                                                                                                    1M0137H02F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0137H02 F, genomic survey sequence.
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Insert Length: 10000 Std Erro
Plate: 0003 row: H column: 2:
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Fax: 801 585 7177
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F/Clone_11b="Mouse 10kb plasmid UUGCIM library" /notee="Vector: pWp42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No.
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1M0164P21F Mouse 10kb plasmid Ut
clone UUGC1M0164P21 F, genomic s
AZ398873
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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Insert Length: 10000 Std Erro
Plate: 0137 row: H column: 0
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Tel: 801 585 5606
Fax: 801 585 7177
                      plasmid inserts
                                           Mouse whole genome scaffolding with paired end reads from 10kb
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Contact: Robert B.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
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UUGC1M library Mus musculus genomic
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                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
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plasmid inserts
Unpublished (2000)
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 23)
                                                                                                                                                                                                                                                                                                                       AZ439451.1 GI:10563464 GSS.
                                                                                                                                                                                                                                                                  Mus musculus
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Insert Length: 10000 Std Err
Plate: 0164 row: P column: 2
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWm92 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Pred. No. 1.6e+03;
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1M0487M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0487M05 R, genomic survey secuence
AZ632757
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Insert Length: 10000 Std mror:
Plate: 0230 row: C column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                  plasmid inserts
Unpublished (2000)
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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University of Utah Genome Center
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                             Contact: Robert
                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC1M0230C09"
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/strain="C57BL/6J"
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Pred. No. 1.6e+03;
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Insert Length: 10000 Std Error: |
Plate: 0487 row: M column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                           GSS.
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population
                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                            Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Fax: 801 585 7177
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                                                                    Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                              Direct Submission
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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AZ812579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunnægenetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0079 row: A column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Meanen, E., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse, Whole genome scaffolding with paired end reads from 10kb Mouse, Whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone UUGC2M0079A23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2M0079A23F Mouse 10kb plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to give a right size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ812579.1 GI:12981965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ812579
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                                                                                                                                                                                                                                                                                                               quality sequence stop: 24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCM library"/note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0079A23"
                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="229c12"
                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                      location/Qualifiers
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Pred. No.
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UUGC1M library Mus musculus
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DEFINITION
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0228 row: A column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
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                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
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                   /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
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Laboratory Mouse DNA Resource
                                                                                                                                                                                                       mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                  sex="Male"
                                                                                                                                                           db_xref="taxon:10090"
clone="UUGC1M0228A10"
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Pred. No. 1.7e+03;
0; Mismatches 5
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VERSION KEYWORDS

ACCESSION

AZ438069

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SOURCE

ORGANISM

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FEATURES

(http://www.jax.org/resources/documents/dnares/). The DNA

COMMENT

JOURNAL TITLE

Query Match Best Local Similarity

0.2%;

DB 1; Length 24;

Query Match Best Local :

Local Similarity

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REFERENCE
AUTHORS
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VERSION
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AZ764496
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                                                                                                                                                                                                                                                                                                                                                                  Plate: 0560 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R.,

Nidechausern, A. and Wright, D., Weiss R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 bp DNA linear GSS 16-FEB-2011M0560H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560H02 R, genomic survey sequence.
AZ764496
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 02
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                                                                       /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20
Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a
                                                                                                                                                                    sex="Male"
                                                                                                                                                                                           clone="UUGC1M0560H02"
                                                                                                                                                                                                                                 mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                              _xref="taxon:10090"
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Pred. No. 1.7e+03;
0; Mismatches 5
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWPA2 (gi|4732114 gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 0.2%; Score 15; DB 1; Pred. No. 1.7e+03; Length 24;

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."

VERSION KEYWORDS SOURCE 片 ঠ FEATURES COMMENT REFERENCE ACCESSION DEFINITION POCUS RESULT 1490 AZ764513 Matches TITLE AUTHORS ORGANISM JOURNAL source 4021 AAAAAGAGAGAAAACAAAATGTT 4043 18;  $\vdash$ Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Nouse whole genome scaffolding with paired end reads from 10kb Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: | Plate: 0560 row: D column: 11 Seg primer: CACACAGGAAACAGCTATGACC Contact: Robert B. University of Utah University of Utah plasmid inserts Unpublished (2000) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24) Mus musculus (house mouse) AZ764513.1 GI:12879553 GSS. 1M0560D11R Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0560D11 R, genomic survey sequence. Class: plasmid ends
High quality sequence stop: 24. Tel: 801 585 5606 Fax: 801 585 7177 AZ764513 AZ764513 AAAAAAAAAAAAAAAATTTT 23 . 308, USA Conservative Biomedical Polymers Research Bldg., (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F./clone lib="Mouse 10kb plasmid UUGCLM library" /note="Vector: PWD42nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jack Laboratory Mouse DNA Resource /db\_xref="taxon:10090" /clone="UUGC1M0560D11" /mol\_type="genomic DNA" /strain="C57BL/6J" organism="Mus musculus" ocation/Qualifiers sex="Male" Weiss Genome Center ٥, Std Error: 0.00 Mismatches mid UUGCIM library Mus musculus Indels 20 S. 2030 from the Jackson GSS 16-FEB-2001 Murinae; Mus. 0 ; ¤ Gaps genomic The DNA SLC, ۳. ت S 0

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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Weenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ448207 24 bp DNA linear GSS 04-OCT-20
1M0245E16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0245E16 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 24.
Location/Qualifiers
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/lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
//lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
//clone lib="Mouse 10kb plasmid UUGCIM 11brary"
//note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C578L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through &
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="qenomic איז"
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0245E16"
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                  'sex="Male"
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Pred. No. 1.7e+03;
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KEYWORDS

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FEATURES

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Pocus

SOURCE

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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ACCESSION
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KEYWORDS
                                                                                                                                                                RESULT 1493
CF301712/c
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Oryza sativa
Oryza sativa
                                                                                                  CF301712 25 bp mRNA linear TLEAF--06-K21.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--06-K21, mRNA sequence.
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                                                              CF301712.1
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1 (bases 1 to 25)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL048782 25 bp mRNA linear EST 04-S: DKFZp5660013_r1_566 (synonym: hfkd2) Homo sapiens cDNA clone
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                                                 /clome="DKFZp5660013"
/tissue_type="kidney"
/dev_stage="fetal"
/dev_stage="fetal"
/lab_host="x1-2blue"
/clome_lib="566 (symonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                              GI:33673473
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ832800 25 bp DNA linear GSS 20-FEB-20 2M0113M21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0113M21 F, genomic survey sequence.
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Ehrhartoideae; Oryzeae; Oryza.
                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0113 row: M column: 21
                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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Location/Qualifiers
                                                              Class: plasmid ends
                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                quality sequence stop: 25.
Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="R.ice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="7LEAF--06-K21"
/tissue_type="leaf"
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/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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ORGANISM
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AL587648/c
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Best Local :
                                                                                                                                                source
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1 (bases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (chicken)
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EST.
                                                                                                                                                                                        Seq primer: M13F.
                                                                                                                                                                                                                                       Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTT 3' Po
                                                                                                                                                                                                                                                                                                                                                                                     Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP Chicken Brain Library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROS060C07, mRNA sequence.
AL587648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF329072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                               /organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0113M21"
/tissue_type="Brain"
/dev_stage="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                    ocation/Qualifiers
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AZ381039
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Insert Length: 10000 Std Erro
Plate: 0137 row: N column: 18
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Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
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University of Utah Genome
University of Utah
Rm. 308, Biomedical Polyme
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Location/Qualifiers
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymcleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4733114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"/clone_"Vector: PWD42nv; Purified_genomic_DNA_from_M./note="Vector: PWD42nv; Pwd42n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0137N18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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Pred. No. 1.8e+03;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0146 row: A column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 25)
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High quality sequence stop: 25.
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah University of Utah
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was bight the constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pDM42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XII0-Gold, T1-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PW042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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25 bp mRNA linear EST U6-FKB-L9 yb08h08.sl Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70623 3' similar to similar to gb.X62744 CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Tel: 81-298-53-4664
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Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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AU265663 VS Dictyostelium
 Hillier, L., Lennon, G.,
                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Hideko Urushihara
Institute of Biological Sciences
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="mat A"
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clone="VSF713"
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Pred. No. 1.8e+03
Becker, M., Bonaldo, M.F., Chiapelli, B.,
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Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hin Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and mhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockwille, MD. Genomic DNA isolated from a cloned population
                                                                                                                           Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                             Trypanosoma brucei
                                                                                                                                                                                                                                                                                   SSD
                                                                                                                                                                                                                                                                                                                                     T. brucei sheared genomic
genomic survey sequence.
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High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Other_ESTs: yb08h08.rl
Contact: Wilson RK
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Genome Res. 6 (9), 807-828 (1996)
97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                   AL451366.1 GI:11833388
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/mol_type="mRNA"
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Pred. No. 1.8e+03;
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       Query Match 0.:
Best Local Similarity 78.:
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL587774
AL587774.1 GI:13192808
EST.
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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/mol type="genomic DNA"

/strain="TREU927"

/db xref="taxon:5691"

/clone="12f02"
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"" wiematches 5; Indels
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   Score 15; DB 1; Le
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Gallus gallus cD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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Fax: 801 585 7177
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0170 row: J column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308,
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0170J19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male"
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Matches Query Match

18;

Conservative

0;

Mismatches

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Gaps

0

78.3%; 0.2%;

Score 15; I Pred. No. 1.

DB 1; .9e+03; 5;

Length 27; Indels

Local Similarity

4039

CF333518/c

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26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 367 Std Error: 0.00
                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R31539.1 GI:787382
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                                                                                           Similarity
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                                  GAGAAAAAGAGAGAAAACAAAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 286 1800
314 286 1810
                                                                         Conservative
                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:541217"
/db_xref="taxon:9606"
                                                                                                                                               constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:135296"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa; Chordata;
Eutheria; Primates;
                                                                                       0.2%;
                                                                       0
                                                                     Score 15; DB
Pred. No. 1.9e
0; Mismatches
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                                                                                                            DB 1;
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                                                                                                        Length 27;
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Tan,F.,
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RESULT 1504

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CF311022/c
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CF311022.1
EST.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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JMT--02-H05.g1 AtJMT-overexpressing transgenic rice library (JMT) Oryza sativa cDNA clone JMT--02-H05, m
                   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                       CF311022 27 bp mRNA linear EST 15-AUG-2003
ABF--06-B07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-B07, mRNA sequence.
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CF333518.1 GI:33815326
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                  Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nahm B.H.
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Location/Qualifiers
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/mol type="mRNA"
/culTivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--02-H05"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="AtDMT-overexpressing transgenic rice
cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyltransferase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DB 1;
Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27
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plasmid cDNA
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                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0331 row: E column: 1
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ495352 27 bp DNA linear GSS 05-OCT-20
1M0331E14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0331E14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                         Plate: 0331 row: E column: 14 Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
Unpublished (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GSS.
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                                                                                                                                                                                                            quality sequence stop: 27.
Location/Qualifiers
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Location/Qualifiers
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical
                                                                                                                        organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0331E14"
                                                                 ′sex="Male"
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/mol_type="mRNA"
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/clone="ABF--06-B07"
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Pred. No. 1.9e+03;
0; Mismatches 5
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JOURNAL COMMENT
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AZ953355/c
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AUTHORS
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ORGANISM
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.1
Plate: 0218 row: M column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
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Mouse whole genome scaffolding with paired end reads from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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                                                                                                                                                                                                                                                                                                         High quality sequence stop: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
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GSS.
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/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant,
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Tyector: PWD42ny; Purified genomic DNA from I
musculus C57BL/6J (female) was obtained from the
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                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                clone="UUGC2M0218M01"
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78.3%;
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Pred. No. 1
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AL587605/c
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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AL587605
AL587605.1 GI:13192639
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Roslin, Midlothian, EH25 9PS, UK
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GCGGCCGCTTTTTTTTTTTTTTTTT 3' Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
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BP Chicken Brain Library
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    Conservative
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                                                                                                                                              /tissue_type-____/dev_stage="Unknown"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP_Chicken_Brain_Library"
/clone_lib="BP_Chicken_Brain_Library"
/note="Vector: psPORT1; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Olīgo dT. 5; adaptor sequence: 5; TCGACCTCGAG 3; 3; adaptor sequence: 5;
5; TCGACCTCGAG 3; 3; adaptor sequence: 5;
6; TCGACCTCGAG 3; 3; Adaptor sequence: 5; Brain adaptor sequence: 5; Brai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="Brain"
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Score 15; DB 1;
Pred. No. 2e+03;
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29 bp mRNA linear EST 07-MAR-1995 ya52f07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66565 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16 PRECURSOR (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High qality sequence starts: 1
High qality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
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Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clome lib="Soares fetal liver spleen iNFLS"
/clome lib="Soares fetal liver spleen iNFLS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
/note="Organ: Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AU267990
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                                                                                                                                                                                                                                                                             Takeuchi,I., Kohara,Y. and Tanaka,Y. Population analysis of cDNAs from unicellular and multicellular stages of Dictyostellum discoideum Unpublished (2002)
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Dictyostelium discoideum
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 29)
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AU267990 VS Dictyostelium
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                                                                                                                                                                                                         Tel: 81-298-53-4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 29)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
                                                                                                                                                                            Email:
                                                                                                                                                                                                                                    University of Tsukuba
                                                                                                                                                                                                                                            Institute of Biological Sciences
                                                                                                                                                                                                                                                                 Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                    Urushihara, H., Morio, T., Saito, T., Koriki, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                     Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                         hideko@biol.tsukuba.ac.jp
                         /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                 /mol_type="mRNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                           Bex="mat A"
                                                                     clone="VSH801"
                                                                                      db_xref="taxon:44689"
                                                                                                                                organism="Dictyostelium discoideum"
                                                                                                                                                             ocation/Qualifiers
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dev_stage="fetal"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                            Gallus gallus
                                                                                                                                                                                                          AL588429 BP Chicken Brain
ROS072C03, mRNA sequence.
                                                                                                                  Gallus gallus (chicken)
                                                                                                                                                                                                                                                              AL588429
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and phl@sanger.ac.uk
                                                                                                                                                                   AL588429.1 GI:13193463
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/clone="244g08"
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/strain="TREU927"
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                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0181 row: I column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 bp DNA linear GSS 21-FEB-20
2M018II07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M018II07 R, genomic survey sequence
                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Contact: Frazer Murray
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Unpublished (2000)
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                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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1 (bases 1 to 32)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                         quality sequence stop: 32.
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/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="PH10B"
/lab_host="PH10B"
/clone_lib="BP_Chicken Brain Library"
/clone_lib="BP_Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: OlTgo dT. 5' adaptor sequence:
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS072C03"
/organism="Mus musculus"
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University of Wales,
Bangor LL57 2UW
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                                                                                                                                                                                                                                                                            Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                    Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
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Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hippoboscoidea; Glossinidae; Glossina
1 (bases 1 to 32)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                               clones with suffix qlc are reverse primer reads starting of the cDNA all plc reads are from 3^\prime end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=\overline{^{n}}Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
organism="Glossina morsitans morsitans"/
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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/note="Vector: PWD42nv; Purified genomic DNA f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0181I07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
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; Pred. No. 2.1e:
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 10-OCT-2003
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RESULT 1516
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MEDLINE
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Matches 18; Conser
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Best Local Similarity
Matches 18; Conserv
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Bangor LL57 2UW
All clones with suffi
end of the cDNA all p
the 3' end.
\omega
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX564081 GI:33431278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX564081 linear KST 10 BX564081 Glossina morsitans morsitans adult infected gut G morsitans morsitans cDNA clone Tse6f01_plc, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response genes
Genome Biol. 4 (10), R63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Hall N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     morsitans morsitans
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llarity 78.3%;
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                                                                          Conservative
                                                                                                                                                       T.brucei"
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T.brucei"
                                                                                                                                                                                                                                                                                                    /organism="Glossina morsitans
/mol_type="mRNA"
                                                                                                                                                                                                       /clone="Tse6f01 p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo
                                                                                                                                                                                                                                                                    /sub_species="morsitans"
/db_xref="taxon:37546"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="morsitans"
/db_xref="taxon:37546"
                                                                                                                                                                       note="country: Zimbabwe; EST from adult gut infected with
                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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78.3%;
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Pred. No. 2.1e+03;
0; Mismatches 5;
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                                                                                          Score 15;
Pred. No.
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2003)
                                                                                            DB 1; 1
2.1e+03;
                                                                                                                                                                                                                                                                                                                              morsitans"
                                                                          .
                                                                                                            Length 33;
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                                                                                                                                                                                                         morsitans adult infected
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RESULT 1518
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AW246505
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was
                                                                                                                                                                                                                                                       4464
CF329020

18 bp mRNA linear EST 18-AUG-2003
NACL--04-D03.bl Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence
                                                                                                                                                                                                                                                                                                              16;
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1 (bases 1 to 18)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Other ESTs: 2821585.5prime
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High
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Plate: LLCM7 row: D
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2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
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                                                                                                                                                                                                                                                                                                                                                                                                              /Cell lime="MGC3"
/lab Host="PHOUS"
/clone_lib="NHLM_MGC_7"
/clone_lib="NHLM_MGC_7"
/note="Organ: lung; Vector: poTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/KhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821585"
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Pred. No. 1.
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AI371092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 bp mRNA linear EST 16-FEB-199 similar to TR:\(\overline{Q}\)26195 Bxn23 Homo sapiens cDNA clone IMAGE:2043424 3' similar to TR:\(\overline{Q}\)26195 PVA1 GENE. ;contains L1.b3 L1 repetitive element ;, mRNA sequence.
Al371092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                         1 (bases 1 to 19)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurola

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index

(CGAP/BTGAP), Tumor Gene Index

(Onpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                         Bonaldo,
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
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                                                                                                                                                       Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI371092.1 GI:4149845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com,
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                                                                                                           cDNA Library Preparation: M. Bento
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82 31 321 6355
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E_coli_DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--04-D03"
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Pred. No. 1.1e+03;
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                                                                                                           Soares,
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                                                                                                           Ph.D.,
                         Sequencing Center information can be
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CF309858/c
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Best Local Similarity 88.9%;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                             Email: bhnahm@ggbio.com, bhn
Location/Qualifiers
                                                                                                                                                                                                                                                                                Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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CF309858.1 GI:33681619
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                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and
                                              /organism="Oryza sativa"
/mol type="mrNA"
/mol type="mrNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xxef="taxon:4530"
/clone="ABF--04-D16"
/tissue_type="ladf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_11b="ABF3-overexpressing transgenic rice plasmid
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn23"
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/db_xref="taxon:9606"
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Pred. No. 1.2e+03;
0; Mismatches 2;
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Best Local Similarity
Matches 16; Conserv
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AZ789309.1 GI:12929974 GSS.
Mus musculus (house mou
                                                                    AZ789309 19 bp DNA linear GSS 14 2M0036L22R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0036L22 R, genomic survey sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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EST.
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Similarity 88.9%;
musculus (house mouse)
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Location/Qualifiers
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/db_xref="taxon:4530"
/clone="JMT--08-C02"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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/lab_nost="E.coli DH10B"
/clone lib="AttNT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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/mol_type="mRNA"
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Pred. No. 1.2e+03;
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Matches 16; Conserv
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                                               AU007655
AU007655.1
EST.
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AU007655 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc02339, mRNA sequence.
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Schizosaccharomyces pombe
Schizosaccharomyces pombe
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Nouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: L column: 22
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resources (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                        USA
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strain="C57BL/6J"
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Pred. No. 1.2e+03;
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                       (fission yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \vdash
                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: B column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
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                  High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                 University of Utah Genome 
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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Morimyo, M. and Mita, K.
                                                              Class: plasmid ends
                                                                                   Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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/clone="spc02339"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
"ha world wide web. (URL, http://www.nirs.go.jp)"
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/mol_type="mRNA"
/strain="972"
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1M0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0208L05 R, genomic survey sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                          High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0208 row: L column: 05
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                    University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 20)
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                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
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                                                                                               Class: plasmid ends
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(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pND42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                  USA
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 1.
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2;
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Best Local (
                                                           source
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                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: G column: 11
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                       Class: plasmid ends
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                                                                                                              quality sequence stop: 20.
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                                                                                                                                                                                                                                                                                                                                  USA
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/organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                    Location/Qualifiers
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AZ943793/c
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ORGANISM
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VERSION
KEYWORDS
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                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0204 row: A column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                             High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2M0204A07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0204A07 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                        USA
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0574G11"
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Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: N column: 07
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1M0212N07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0212N07 R, genomic survey sequence.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pM942nv, Purified genomic DNA from M.
musculus_C57BL/6J (female) was obtained from the Jackson
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                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                     Location/Qualifiers
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                                                                           organism="Mus musculus"
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xref="taxon:10090"
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Pred. No. 1.3e+03;
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clone="UUGC1M0250D13"

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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                               Tel: 801 585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0250 row: D column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                       High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                       84112,
                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: FWD42nv; Purified genomic DNA from
                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0212N07"
                                                                      organism="Mus musculus"
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Pred. No. 1.
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Best Local (
                                                                                                                                 source
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                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0358 row: B column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1M0358B07F Mouse 10kb plasmid UUGC1M library Mu clone UUGC1M0358B07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                       quality sequence stop: 21.
Location/Qualifiers
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                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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db_xref="taxon:10090"
clone="UUGC1M0358B07"
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Pred. No. 1.5e+03;
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AZ995847
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Best Local Similarity
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                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: N column: 16
Seq primer: CACAAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R. Mouse whole genome scaffolding with paired end reads from 10kb Nouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                         High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        84112,
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AZ995847.1
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21 bp DNA linear GSS 27
200281N16R Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0281N16 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGGGGGGTGGGAGTG 1
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
"\".''.'note="Vector: PWD427w; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                   mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                   clone="UUGC2M0281N16"
                                                                             db_xref="taxon:10090"
                                                                                                                                                      organism="Mus musculus
lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:13867074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 1;
Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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22 bp mRNA linear EST 04-JUN-1999 as34g10.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE 2319138 3' similar to TR:062106 Q62106 PROLINE-RICH SALIVARY PROTEIN ; contains element MSR1 repetitive element ; mRNA sequence. AI707945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU, NCI human EST Project Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 22)
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                                                                                                                                                                                                                                                                                                                            quality sequence stop: 1.
Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pNR042 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
/nusculus C57BL/6J (female) was obtained from the Jackson
/dev_stage="adult, age 64"
/lab_host="PH10B (phage resistant)"
/clone lib="Barstead aorta HPLRB6"
/note="Organ: aorta; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2319138"
                                                                                                                                       sex="male"
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Pred. No. 1.5e+03;
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AI707945

SOURCE KEYWORDS VERSION

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FEATURES

Query Match Best Local Similarity

88.9%;

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AI738599
AI738599
ARNA linear EST 21-DEC-19
Wi39902.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2392658 3'
Similar to SW:MNT_HUMAN Q99583 MAX BINDING PROTEIN WNT ; contains
MER22.t1 MSR1 repetitive element ;, mRNA sequence.
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1 (bases 1 to 22)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 383 Std Err
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality Insert Length: 383 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                              Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2392658"
                                                                                                                                                                                                                                                                                                                                         tissue_type="colon tumor, RER+"
'lab_host="DH108"
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Score 14.8; D
Pred. No. 1.6e
0; Mismatches
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Pred. No. 1.6e+03;
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                                          Length 22
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AZ307559
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: O column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
Rm. 300, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
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GSS.
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                                                                                                         / Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ (clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaixed with T4 DNA polymerase and T4
polymuleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi[4732114]gb[AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competents. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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                           88.9%;
                                                      0.2%;
                           Score 14.8; DB 1;
Pred. No. 1.6e+03;
                                                      Length 22;
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RESULT 1535
AZ345528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Insert Length: 10000 Std Err
Plate: 0080 row: N column: 0
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi |4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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'strain="CS7BL/6J"
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0.2%;
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Conservative

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Mismatches

Length 22;

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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                                                   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R. Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., H. Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                T. brucei sheared genomic genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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Trypanosoma brucei
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T. brucei sheared genomic
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Trypanosoma brucei
                                                                                                                                  Trypanosoma.
                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/clone="214d07"
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/strain="TREU927"
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Pred. No. 1.
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1.6e+03;
ches 2;
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                    Query Match
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
  l Similarity
19; Conserv
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Details of T. brucei sequencing at the Sanger Centre
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Edge BioSystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 26)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
plate: LLCM0028 row: C column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW327613
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/db_xref="taxon:9606"
/clone="IMAGE:2846536"
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/clone="282d06"
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                                                                                                /clone_lib="NIH_MGC_2"
/note="Organ: Blood; V
                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                          tissue_type="T cell leukemia"
cell_line="MGC2"
                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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Pred. No. 1.6e+03;
0; Mismatches 2;
                    Score 14.8;
Pred. No. 26
    Mismatches
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sapiens
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                       2e+03;
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cDNA clone
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ne IMAGE:2846536 3',
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                                                               Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H
Large-scale Sequencing Analysis of Rice EST
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CF282426
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Fax: 82 31 321 6355
                                                                                                                                                   Oryza sativa
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                                                     (bases 1 to 26)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kyeonggi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="148TL--04-D22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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73.1%;
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Pred. No. 2e+03;
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                                  Lee, T.H., Shin, Y.C.,
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Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                               Email: bhnahm@ggbio.com,
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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                                                                                                                                                                                      organism="Oryza sativa"
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/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                             bhnahm@bio.myongji.ac.kr
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Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
1 (bases 1 to 26)
1 (Xim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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7LEAF--08-M19.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--08-M19, mRNA sequence.
CF302874
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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CF299701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 2e+03;
D; Mismatches
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RESULT 1544
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Best Local Similarity
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lo

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-J01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                     Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA_was_capped_with_oligoribonucleotides_and_then_used_as_templates_for_pCR."
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried force="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried force="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried forces"
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
for 2hrs. Oligo-capped mRNA was reverse transcribed and
                                                                                                                                                               /db_xref="taxon:4530"
/clone="ABF--06-J01"
                                                                                                                                                                                                        organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2e
                                                                                                                                                                                                                                                                                                                               bhnahm@bio.myongji.ac.kr
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                                                                                                                  AZ359871 26 bp DNA linear GSS 02-OCT-200100102H23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0102H23 R, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                           AZ359871.1 GI:10473571
GSS.
                                                                                                   AZ35987
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Similarity 73.1%;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol type="mRNA"
/culTivar="Nackdong"
/db xxef="taxon:4530"
/clone="NACL--07-J02"
                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                              AZ376664 26 bp DNA linear GSS 02
1M0130B08R Mouse 10kb plasmid UUGC1M 11brary Mus musculus
clone UUGC1M0130B08 R, genomic survey secuence
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1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                  Mus musculus
                                                                                                                            AZ376664.1 GI:10490364
                                                                              Mus musculus (house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0102 row: H column: 23
Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
//sex="Male"
//lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
//clone_lib="Mouse_likb plasmid_UUGCIM_library"
//note="Pwector: PWD42rv, Purified_genomic_DNA_from_M.
musculus_C57BL/6J (male) was obtained_from_the_Jackson
Laboratory Mouse_DNA_Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4_DNA_polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high_molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector_DNA, was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible_derivative_of_plasmid_R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse_DNA was annealed to
adaptored vector_DNA, and transformed_into
chemically-competent_B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/mol_type="genomic_DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                              mouse)
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Pred. No. 2e+03;
0; Mismatches 7;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                            26 bp DNA linear GSS 02-OCT-20 1M0150D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150D13 R, genomic survey sequence.
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Plate: 0130 row: E column: 08
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 26)
                                                                             Mus musculus
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Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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1M0189M07F Mouse 10kb plasmid clone UUGCIM0189M07 F, genomic
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                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0150 row: D column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                           AZ414673.1 GI:10538686
GSS.
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                             AZ593300 26 bp DNA linear GSS 13-DEC-2001000404E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0404E16 R, genomic survey sequence.
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Insert Length: 10000 Std Erro
Plate: 0189 row: M column: 07
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Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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ligated to the blunt ends in high molar excess. The
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electrophoresis. Vector DNA was prepared from a derivative
of pWD2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0189M07"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 2e+03;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
IBlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 26)
                                                                                                                                                                                                                                           1M0439E17R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0439E17 R, genomic survey sequence.
                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                             AZ612722
                                                                                                                                                     Mus musculus (house mouse)
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Insert Length: 10000 Std Err
Plate: 0404 row: E column: 1
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University of Utah Genome Center
University of Utah
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Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Pred. No. 2e+03;
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Reilly, M., Rose, M., Rose, R., Stokes, R.,

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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: E column: 17
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University of Utah Genome Center
University of Utah
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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1M0463G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0463G07 F, genomic survey sequence.
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Niederhausern, A. and Wright, D., Weiss, R.
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/strain="C57BL/6J"
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  TITLE
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University of Utah Ge
University of Utah
Rm. 308, Biomedical F
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                                                                                                                                                                                                                                                                                                   AZ627846 26 bp DNA linear GSS 13 1M0474H08F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0474H08 F, genomic survey sequence.
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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High quality sequence stop: 26.
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Insert Length: 10000 Std Erro
Plate: 0463 row: G column: 0
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Fax: 801 585 7177
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                      AZ627846.1 GI:11750132 GSS.
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Unpublished (2000)
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/clone_lib="Mouse 10kb_plasmid_UUGC1M_librarv"
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/strain="C57BL/6J"
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| Wector: PWD42nv; Purified genomic DNA from M.
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Matches 19; Conserv
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Tel: 801 585 5606
Fax: 801 585 7177
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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High quality sequence stop: 26.
Location/Qualifiers
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1 (bases 1 to 26)
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Insert Length: 10000 Std Error:
Plate: 0474 row: H column: 08
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Contact: Robert B.
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/strain="C57BL/6J"
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Pred. No. 2e+03;
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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Insert Length: 10000 Std Erro
Plate: 0525 row: H column: 1
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coil XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0525H15"
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/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: O column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                   2M0233N01F Mouse 10kb plasmid clone UUGC2M0233N01 F, genomic
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Fax: 801 585 7177
                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                          Mus musculus
Contact: Robert B. Weiss
                          Unpublished (2000)
                                               plasmid inserts
                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNAP2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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/strain="C57BL/6J"
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Insert Length: 10000 Std Erro
Plate: 0233 row: N column: 01
                                     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
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High quality sequence stop: 26.
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Fax: 801 585 7177
Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                              Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                             Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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T. brucei sheared genomic DNA
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                         nh1@sanger.ac.uk
                                                                                                                Direct Submission
                                                                                                                                                                                                                       Trypanosoma.
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from l
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Matches 19
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                                                                                                                                                                                                                                                                                                                        riace: 0094 row: D column: 14 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid anda
                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0094 row: D column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 bp DNA linear GSS 02-OCT-201
1M0094D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0094D14 R, genomic survey sequence
A2355083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotpun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
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GSS.
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                                                                                                                                                                                                                                                                                              quality sequence stop: 26.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"/clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0094D14"
                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                     'sex="Male"
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/clone="324d07"
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Pred. No. 26
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Matches 19 4013 AAATGAGAAAAAAAGAGAGAAAAACAAA 4038 19; Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., plasmid inserts Unpublished (2000) Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Erro Plate: 0460 row: L column: 0: Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@gene AZ623156 26 bp DNA linear GSS 1: 1M0460L01R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC1M0460L01 R, genomic survey sequence. Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus 1 (bases 1 to 26) Mus musculus (house mouse) AZ623156.1 GI:11745346 Similarity AAAAAAAAAAAAATAAAAAAAAAA 26 lass: plasmid ends lgh quality sequence stop: 26. Location/Qualifiers Conservative (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pND42 (gi|4732114|gb|AFT29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and USA /lab\_host="E. Coli strain XL10-Gold, T1-resist. /Clone\_lib="Mouse 10kb plasmid UUGC1M libzay" /note="Vector: pwD42nv; burified genomic DNA f musculus C57BL/6J (male) was obtained from th purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance." /organism="Mus musculus" /mol\_type="genomic DNA" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="UUGC1M0460L01" Laboratory Mouse DNA Resource sex="Male" 0.2%; 0; Score 14.8; DB 1; Length 26; Pred. No. 2e+03; Std Error: 0.00 Mismatches 2e+03; 7; 20 T1-resistant, ŝ 2030 <u>,</u> from M. ; ; Gaps SLC, 5 0;

REFERENCE AUTHORS

COMMENT

JOURNAL TITLE

FEATURES

source

from the Jackson

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION

RESULT 1559 AZ623156/c

DEFINITION

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RESULT 1560
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26 bp mRNA linear EST 15-AUG-20
ABF--04-F09.gl ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--04-F09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
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Unpublished (2003)
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82 31 330 6193
82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                          /dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-F09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa"
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                         Score 14.8; DB 1; Length 26; Pred. No. 2e+03;
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Pred. No. 2e+03;
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                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 27)

1 (bases 1 to 27)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                               AZ970621.1 GI:13841848 GSS.
                                                                                                                                                                                                                                                                                                   2M0243N14R Mouse 10kb plasmid clone UUGC2M0243N14 R, genomic
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Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: David L. Adelson
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1 (bases 1 to 26)
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Contact: Robert B.
               Unpublished (2000)
                                   plasmid inserts
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                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAAAAAAGAAAAAA 1
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN. ...NNNinsert) GCGAATTGGACCTCCACGCGGTGGCGGCGGCGCGGCTGACCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mol type="mbNA"
/db xref="taxon:9823"
/dev stage="fettal"
/clone_lib="CSEQFXL36 fetal brain"
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 Weiss
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genomic survey sequence.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Fax: 4dunn@genet
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and Marra, M. Generation and analysis of 280,000 human expressed sequence tags.
                                          Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiapee, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, W., Le, M., Le, N., Le, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                               2/ pp mRNA linear EST 30-JAN-1: yz02d07.sl Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGE:281869 3/ similar to gb:M85164 SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 27)
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Insert Length: 10000 Std Bror: I
Plate: 0243 row: N column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                        N51845.1
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducable derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                      GI:1193011
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Female"
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|strain="C57BL/6J"
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Pred. No. 2e+03;
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                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Prange,C., Rifkin,L., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Mardis,E., Moore,B., Morris,M., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,B., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                  752836 28 bp mRNA linear EST 06-
ya81b09.s1 Stratagene ovary (#937217) Homo sapiens cDNA clu
IMAGE:68057 3' similar to similar to gb:X53463 GLUTATHIONE
PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
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Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996) 97044478
                                                            and Marra, M.
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; lst_strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:3900397"
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/mol_type="mRNA"
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Pred. No. 2e+03;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0091 row: A column: 1
                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ819924 29 bp DNA linear GSS 20-FEB-200200091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC2M0091A19 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 51 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                   Mammaila; Futheria; Rodentia;
1 (bases 1 to 29)
Junn, D., Aovari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -21m13
High quality sequer
                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                 plasmid inserts
                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAACAAAAAAAAAAAAAAAAAA 1
te: 0091 row: A column: 19
primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                        308,
                                                                                      801 585 5606
801 585 7177
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Location/Qualifiers
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                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGGCACCAG 3' ~3' adaptor sequence: 5'
                                                                                                                                                      Biomedical Polymers Research Bldg.,
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|mol_type="mRNA"
|db_xref="GDB:504314"
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Pred. No. 2.1e+03;
0; Mismatches 7;
                                         Std Error: 0.00
                                                                                                                                                                                                 Center
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7;
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AZ492630/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ492630 29 bp DNA linear GSS 0: 1M0326B22R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC1M0326B22 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0326 row: B column: 22
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS
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                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                              University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ492630.1 GI:10665537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 26
                                                                                                                                                                                                                                                                                                       308,
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                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC2M0091A19"
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Pred. No. 2.1e+03;
                                                                                           Std Error: 0.00
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RESULT 1567
CF295451/c
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AUTHORS
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DEFINITION
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JOURNAL
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 29)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 bp mRNA linear EST 14-AUG-:
30DGS--05-G15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
8ativa cDNA clone 30DGS--05-G15, mRNA sequence.
CF295451
                                                                                                                                                                                                                                 Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF295451.1 GI:33664484
EST.
                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
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Location/Qualifiers
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                                                                                                                                                                                bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                        /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/clone="30DGS--05-G15"
/tissue_type="leaf"
                                                     db_xref="taxon:4530"
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|strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                      Korea
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Pred. No. 2.1e+03;
0; Mismatches 7;
                                                                                                                                                                                                           bhnahm@bio.myongji.ac.kr
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RESULT 1569
CF300706/c
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CF299155/c
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7LEAF--05-E15.b1 Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--05-E15, mRNA sequence. CF300706 CF300706.1 GI:33672467
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7LEAF--03-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--03-B02, mRNA sequence.
CF299155
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Losong,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongIn, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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/lab_host="E.coli_DH10B"
/loone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:4530" /clone="TLEAF-03-B02" /tissue_type="lasf" /tissue_type="lasf" /clone="TLEAF-03-B02" /tissue_type="1 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                    0.2%;
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                                                                                                                                                                                                                                                                                                    Score 14.8; DB 1;
Pred. No. 2.1e+03;
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Pred. No. 2.1e+03;
0; Mismatches 7
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(7LEAF) Oryza
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AUTHORS
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CF295370/c
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                                                                                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, Greendene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 bp mRNA linear EST 14-AUG-2003 30DGS--05-E14.gl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-E14, mRNA sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Ehrhartoideae, Oryzeae, Oryza.
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Similarity 73.1%;
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Location/Qualifiers
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RT-PCR.
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clome_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped
with oligoribonuclectides and Then used as templates for
RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/clone="7LEAF--05-E15"
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Pred. No. 2.1e+03;
                                                                                                                                        bhnahm@bio.myongji.ac.kr
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RESULT 1571
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CF311684/c
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Best Local S
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Best Local Similarity
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1 (bases 1 to 29)
1 (bases 1 to 29)
1 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                   ABF--07-A15.gl ABF3-overexpressing transgenic rice library (ABF) Oryza sativa cDNA clone ABF--07-A15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF293772

29 bp mRNA linear EST 14-AUG-2003
30DGS--03-B05.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--03-B05, mRNA sequence.
CF311684.1 GI:33683445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF293772.1 GI:33662805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                 /dev stage="30 days after germination"
/lab host="B.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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Pred. No. 2.1e+03;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                 Score 14.8; DB 1;
Pred. No. 2.1e+03;
0; Mismatches
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                                      EST 15-AUG-2003 plasmid cDNA mRNA sequence.
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RESULT 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                         31 bp mRNA linear ABF--08-H15.gl ABF3-overexpressing transgenic rice library (ABF) Oryza sativa cDNA clone ABF--08-H15, CF312635 CF312635.1 GI:33684396
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                                                                                                                     Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                    1 (bases 1 to 31)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                              Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Tel: 83
Fax: 83
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
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82 31 330 6193
82 31 321 6355
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                                                                         bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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Location/Qualifiers
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABE3-overexpressing transgenic rice plasmid cDNA lībrary (ABF)"
cDNA lībrary (ABF)"
cDNA coligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
1. .31
/organism="Oryza sativa"
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                                                    location/Qualifiers
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73.1%;
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Pred. No. 2.2e+03;
0; Mismatches 7
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rice plasmid cDNA
-H15, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with auffir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      All clones with suffix qlc are reverse end of the cDNA all plc reads are from the 3' end.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX551140 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tsell6g12_plc, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22881942
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                                                                               /clone
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/note="country: Zimbabwe;
F.brucei"
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/clone_Tib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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Pred. No. 2.2e+03
0; Mismatches
                                   EST from adult gut infected with
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Query Match Best Local Similarity

0.2%;

Score 14.8; Pred. No. 2.

8; DB 1; 2.2e+03;

Length 33;

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VERSION
KEYWORDS
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AUTHORS
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                SOURCE
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                                                             CF2/6638

21 bp mRNA linear EST 14-AUG-2003

14ETL--01-N19.bl Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL--01-N19, mRNA sequence.

CF276638
                                                                                                                                                                                                                                                         l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX566898 Glossina morsitans morsitans adult infected gut Glossina morsitans adult infected gut Glossina morsitans morsitans morsitans morsitans cDNA clone Tse84h03_plc, mRNA sequence.
Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All clones with suffix qlc are reverse end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust
Hinxton, Cambridge, CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                Oryza
                                              CF276638.1 GI:33654024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hall N
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nilarity 73.1%;
Conservative
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 sativa
                sativa
                                                                                                                                                                                                                                                                                                                                                                 /sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse84h03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans moz
                                                                                                                                                                                                                                                                                                                          /note="country: Zimbabwe;
F.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Glossina morsitans morsitans"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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Pred. No. 2.2e
0; Mismatches
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Query Match
Best Local Similarity
Matches 17; Conserv
                                  4019 GAAAAAAGAGAGAAAACAAAA 4039
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Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin,
Tel: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

[ (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                               of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 82 31 330 6193 Fax: 82 31 321 6355
GAAAAAAAAAAAAAAAA
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kyeonggi,
                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxxx1:4530"
/clone="14ETL--01-N19"
                                                                                                                                                     /note="Vector: pCR4-TOPO;
with oligoribonucleotides
RT-PCR."
                                                                                                                                                                                                                                                   tissue type="leaf"
/dev_stage="14 days after germination"
/lab_host="E_coli DH10B"
                                                                                                                                                                                                                (14ETL) "
                                                                                         81.0%;
                                                                                                                0.2%;
                                                                                                                                                                                                                                   lib="Rice etiolated leaf plasmid cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Korea
                                                                         0; Mismatches
                                                                                            Score 14.6; DB 1;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GreenGene Biotech Inc.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MyongJi University
                                                                                                                                                                         Site 1: EcoRI; mRNA was capped and then used as templates for
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                                                                                                                Length
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                                                                                                                21;
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                                                                           Gaps
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Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: Plate: 0412 row: D column: 23 Seg primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends University of Utah University of Utah Rm. 308, Biomedical Unpublished (2000) Contact: Robert B. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welse, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 21) Mus musculus clone UUGC1M0412D23 AZ597932 AZ597932 21 bp DNA linear GSS 13-DEC-201 1M0412D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic High quality sequence stop: 21. Tel: 801 585 5606 Fax: 801 585 7177 plasmid inserts AZ597932.1 GI:11720122 musculus (house mouse) USA Genome Center Weiss Polymers Research Bldg., F, genomic Std Error: survey sequence. 0.00 20 ŝ 2030 GSS 13-DEC-2000 [F] SLC, 5

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TITLE
JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 21)

Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Le
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF280925 21 bp mRNA linear EST 14-AUG-20 14ETL--07-M14.b1 Rice etiolated leaf plasmid cDNA library (14ETL) CTYZA SATIVA CDNA Clone 14ETL--07-M14, mRNA sequence.
                                                                                                                                                                                                                                                                   Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF280925.1 GI:33658311
                                                                                                                                                                                                                                          Email: bhnahm@ggbio.com,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
/organism="Oryza sativa"
/mol type="mRNA"
/culfivar="Nackdong"
/db_xref="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL-07-M14"
/tissue_type="latef"
/tissue_type="latef"
/dev_stage="14 days after germination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'sex="Male"
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Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                          bhnahm@bio.myongji.ac.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee, T.H., Shin, Y.C.,
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: L column: 11
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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ilarity 81.0%;
Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pump42 (gil4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                         /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_
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                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Query Match Best Local

Similarity

0.2%;

Score 14.6; DB 1; Pred. No. 1.6e+03;

Length 21;

맑 ફ with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mola DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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JOURNAL COMMENT
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 21)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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(http://www.jax.org/resources/documents/dnaxes/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 |gb| AFT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PMD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"

mol_type="genomic DNA"

strain="C57BL/6J"
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Best Local Similarity 81.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0195 row: A column: 16
Seq primer: CACACAGGAAACAGCTATGACC
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Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical
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                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv, Purified genomic DNA from I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0195A16"
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/strain="C57BL/6J"
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Pred. No. 1.6e+03;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A.; von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Insert Length: 10000 Std Erro
Plate: 0309 row: A column: 05
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Fax: 801 585 7177
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Unpublished (2000)
Contact: Robert B.
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21 bp DNA linear GSS 0:
1M0309A05R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0309A05 R, genomic survey sequence.
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                                                              musculus C57BL/6J (maile) was obtained from the Jackson Laboratory Mouse DNA Resource:

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with high repert adaptors and size-selector was ligated with high repert adaptors.
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:10090"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
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Pred. No. 1.6e+03;
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AZ499R46
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Insert Length: 10000 Std Error: (
Plate: 0337 row: E column: 23
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308,
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi 4732114 [gb | AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UUGC1M0337E23"
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Genome Center
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Pred. No. 1.6e+03;
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Mismatches
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שניים DVGC1M library Mus musculus genomic
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adaptored vector DNA, and trachemically-competent E. coli

XL10-Gold (Stratagene) cells

COMMENT

TITLE

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REFERENCE
AUTHORS
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AZ583408/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 bp DNA linear GSS 13-DEC-200
1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0378N23 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert
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801 585 7177
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Laboratory Nouse DNA Resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="R. Coli strain XL10-Gold, Tl-resistant, F-"/Clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pMp42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC1M0378N23"
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0397 row: B column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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Dunn, D., Aoyagi, A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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1M0476L04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0476L04 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
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1 (bases 1 to 21)
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h quality sequence stop: 21.
Location/Qualifiers
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        / Nex = "Mail" Coli strain XLIO-Gold, T1-resistant, F-"
/ (clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor Oligonucleotides were
ligated to the blunt ends in high molar excess. The
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electrophoresis. Vector DNA was prepared from a derivative
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adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and salacrad for amnicillin resistrance."
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/strain="C57BL/6J"
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selected for ampicillin resistance.
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Pred. No. 1.6e+03;
0; Mismatches 4
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0.2%; Score 14.6;

DB 1;

Length 21;

Query Match Best Local Similarity

0.2%;

Score 14.6; DB 1; Pred. No. 1.6e+03;

Length 21;

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REFERENCE
AUTHORS
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AZ770188/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0571 row: A column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 21)
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1M0571A12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571A12 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ770188.1 GI:12891111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ass: plasmid ends
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pushed (gi 4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Mouse 10kb-plasmid UUGCIM library"
/note="Vector: pWp82nv; burified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UUGC1M0571A12"
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VERSION
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AZ961893/c
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Query Match
Best Local Similarity
Matches 17; Conserv
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21 bp DNA linear GSS 27-APR-200
2M0230E06R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0230E06 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: E column: 06
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 21.
                                                                                            Laboratory Mouse DNA Resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNAP2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="B, coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pW042nv, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC2M0230E06"
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strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                           0.2%;
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Score 14.6; DB 1;
Pred. No. 1.6e+03;
0; Mismatches 4;
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                                                 Length 21;
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Conservative

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4,

Indels

0

Gaps

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Query Match

Local Similarity 81.0

81.0%;

<u>,</u>

Score 14.6; DB 1; Pred. No. 1.7e+03; 0; Mismatches 4;

Length 22; Indels

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KEYWORDS
SOURCE
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1M0127H16F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0127H16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0127 row: H column: 1
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pw1042nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0127H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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BED0016802 3', mRNA sequence.
AU260373 GI:20327801
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A1439277.1 GI:4303196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                  Bukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (Dases 1 to 22)
Kato, K. and Matoba, R.
                                                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Seq primer: -40UP from Gibco High quality sequence stop: 1.
Generation of expressed sequence tags from mouse brain
                                                                                             Mus musculus
                                                                                                                   Mus musculus (house mouse)
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1 (bases 1 to 22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2134250"
/tissue_type="lymphoma, focell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/clone lib="NCI_CGAP_Lym12"
/clone lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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Pred. No. 1.7e+03;
0; Mismatches 4
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                                                                                                                                                                                                                 22 bp mRNA linear I
cDNA library Mus musculus
                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                        Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                     EST 25-APR-2002
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AZ447246/c
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                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Insert Cength: 10000 Std Error:
Plate: 0244 row: E column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Ja
Tel: 81-743-72-5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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USA
                                                                                                                                                                                                                                                  quality sequence stop: 22.
Location/Qualifiers
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0244E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                         sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="brain"
/clone_Tib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="BED0016802"
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Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: M column: 11
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0273M11R Mouse 10kb plasmid clone UUGC1M0273M11 R, genomic
                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 22.
                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                              /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                         /sex="Male"
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0273M11"
                                                                                                                                                                                                                                mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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Pred. No. 1.7e+03;
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> > was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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AUTHORS
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VERSION
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AZ611419/c
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0437 row: D column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah C
University of Utah
Rm. 308, Biomedical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1M0437D15R Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0437D15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
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                                                                                                                                                                                                                                                                                     quality sequence stop: 22.
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                                 musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
was hydrodynamically sheared by repeated passage through a
                 (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                     clone="UUGC1M0437D15"
                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                               sex="Male"
                                                                                                                                                                     db_xref="taxon:10090"
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Pred. No. 1.7
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Matches Query Match Best Local :

Similarity

81.0%; 0.2%; and selected for ampicillin resistance."

DB 1; 4

Length 22; Indels

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells

Conservative

0; Mismatches Score 14.6; DB 1; Pred. No. 1.7e+03;

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RESULT 1595
AZ766712/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: A column: 03
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ766712
22 bp DNA linear GSS 16-FEB-2001
1M0564A03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0564A03 R, genomic survey sequence.
AZ766712
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                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C578L/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                           clone="UUGC1M0564A03"
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ACCESSION
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0570 row: O column: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                        /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0570018"
                                                                                                                                                                                                                                                                                                                   TOW.
                                                                                                                                                                                                               'sex="Male"
                                                                                                                                                                                                                                                                                        mol_type="genomic
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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Pred. No. 1.7e+03;
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was blunt end-repaired with T4 DNA polymerase and

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2M0010I19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0010I19 F, genomic survey sequence
AZ77660s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: I column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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801 585 7177
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                 sex="Male
                                                                                                                                                                                                                                                                                        clone="UUGC2M0010I19"
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Pred. No. 1.7e+03;
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COMMENT

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/) and through a constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

/lab\_host="E. Coli strain XI10-Gold, T1-resistant, F-" /clone\_lib="Mouse\_lokb\_plasmid\_UUGC1M\_library" /note="Vector: pW042nv; Purified\_genomic\_DNA\_from\_M. musculus\_C57BL/6J\_(male) was obtained\_from\_the\_Jackson\_musculus\_C57BL/6J\_(male) was obtained\_from\_the\_Jackson\_Musculus\_C57BL/6J\_(ma

/db\_xref="taxon:10090" /clone="UUGC2M0014M08"

sex="Male"

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VERSION
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SOURCE
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ778745 22 bp DNA linear GSS 16 2M0014M08F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC2M0014M08 F, genomic survey sequence.
                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0014 row: M column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ778745.1 GI:12908699
GSS.
                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                      Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                   308,
                                                                                                               quality sequence stop: 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214/gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg.,
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                            ocation/Qualifiers
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Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: E column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ868780 22 bp DNA linear GSS 21 2M0180E12R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0180E12 R, genomic survey sequence.
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Fax: 801 585 7177
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GSS.
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Location/Qualifiers
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                                                                                                      /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C578L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
and the constant of the constant
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5
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/mol_type="qenomic DNA"
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/clone="UUGC2M0180E12"
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Pred. No. 1.
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Matches 17
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Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Ercor: C
Plate: 0225 row: J column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGTTGGGGGTAGGGGTGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                               /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (Female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                         'sex="Female"
                                                                                                                                                                                                                                                                                                                                      clone="UUGC2M0225J07"
                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%;
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Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00
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kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWn42 (gil4732114 gb[AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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2M0248C01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0248C01 R, genomic survey secuence
AZ97404£
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: C column: 01
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
High quality sequence stop: 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria;
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801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. col' strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse_10kb_plasmid_UUGC2M_library" /note="Vector: pMp42nv, Purified_genomic_DNA_from_M.musculus_C57BL/6J_(female) was obtained_from_the_Jackson_musculus_C57BL/6J_(female) was obtained_from_the_Jackson_Musculus_C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0248C01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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rocus

AZ380872 23 bp DNA linear GSS 02-OCT-200 1M0137H02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0137H02 F, genomic survey sequence.

GSS 02-OCT-2000

ACCESSION DEFINITION AZ380872/c RESULT 1603

AZ380872

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KEYWORDS
SOURCE
ORGANISM
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TA8C02P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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Best Local Similarity
                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, B-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, WD. Genomic DNA isolated from a cloned population of Rockville, WD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgum sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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                                         3852 TCCTTTTCTCCTTATTCCTCC 3872
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                                                                                   l Similarity
17; Conserv
N
                                                                                                                                                                                                                                                                                                                                Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.B., Rajandream,M.A. and Barrell,B.G.
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AL452598.1 GI:11861142
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T. brucei sheared genomic
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                                                                                                                                                                            /db_xref="taxon:5691"
/clone="8c02"
                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                               organism="Trypanosoma brucei"
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Pred. No. 1.7e+03;
0; Mismatches 4;
                                                                                                             Score 14.6; DB 1;
Pred. No. 1.7e+03;
                                                                                          Mismatches
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DNA clone
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Best Local Similarity
Matches 17; Conserv
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24 bp
1M0361H04F Mouse 10kb plasmid UL
clone UUGC1M0361H04 F, genomic &
AZ514388
AZ514388.1 GI:10695704
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Insert Length: 10000 Std Error:
Plate: 0137 row: H column: 02
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GSS.
Mus musculus (house mouse)
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Unpublished (2000)
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                         / Nexa = "Male" ...
/ lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwm42 (gil4732114|gb)AF129072.1), a copy-number
inductble derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0137H02"
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Pred. No. 1.8e+03;
                                              24 bp DNA linear GSS 05 plasmid UUGC1M library Mus musculus genomic survey sequence.
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AZ485624.1
GSS.
                                                                               AZ485624 26 bp DNA linear GSS 05-OCT-200
1M0313H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0313H11 F, genomic survey sequence.
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Mouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired end reads
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Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (2000)
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High quality sequence stop: 24.
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Fax: 801 585 7177
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/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0361H04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gb |AFR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCNM library" /note="Vector: PW927ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso)
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                                 GI:10651606
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Pred. No. 1.9e+03;
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                                                                                                                                          RESULT 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                             CF639306
D14_A02 Filamentous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0313 row: H column: 1:
                                                                sequence.
CF639306
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Ustilago maydis
                                         CF639306.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome 
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                              AAAAAAGAGAGAAAACAAAAT 4040
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801 585 7177
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="UUGC1M0313H11"
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Rodentia;
                                                                                                     Forced
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                                                                                                                                                                                                                                                                                                                        Score 14.6; DB 1; Length 26; Pred. No. 2.1e+03;
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| Diploid Ustilago maydis
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T52979/c
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T52979.1
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4018 AGAAAAAAGAGAGAAAACAAAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; 1 (bases 1 to 26)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene Expression during Ustilago maydis Diploid Filam
                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                       Other_ESTs: ya82e08.rl
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                    Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chispoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Riikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevsskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
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3359 Mississauga Road North, Mississauga,
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
plate: UTM-UM-D126/7-014-UTM row: 02 co-
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                                                                                                                                                                                                                                                Generation and analysis of 280,000 Genome Res. 6 (9), 807-828 (1996)
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Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRECURSOR (HUMAN), mRNA sequence.
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/cell type="Mycella"
/dev_stage="Filamentous diploid"
/dev_stage="Filamentous Forced Diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:654839
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/mol_type="mRNA"
/strain="FBD12"
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Pred. No. 2.1
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                                                                                    Louis,
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JOURNAL COMMENT
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CF334654/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                     Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.

Genomics and Genetics Institute, Contaction of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JMT--04-A12.91 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-A12, mRNA sequence. CF334654 CF334654.1 GI:33817642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LIMI This clone is available royalty-free through LIMI; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 577 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                        bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                     Organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--04-A12"
                     /tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="AtdWT-overexpressing transgenic rice plasmid cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="49 year old"
/lab_host="SOUR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/clone_stagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI.
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
TotaI ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3'"
note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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/db_xref="GDB:504455"
/db_xref="taxon:9606"
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Pred. No. 2.1e+03;
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, MyongJi University
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N31821
N31821.1
EST.
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30 bp mRNA linear EST 10-JAN-1996
yy17g12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE: 771558 3' similar to gb: X68242 PUTATIVE HIV-1 INDUCED PROTEIN
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                                                     HIN-1 (HUMAN);, mRNA sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                     GI:1152220
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--02-C01"
/tissue_type="leaf"
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Pred. No. 2.2e+03;
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 8
Ehrhartoideae; Oryzeae, Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                           CF317778
CF317778.1 GI:33689539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                              HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cD library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.
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                                                                                                 Oryza sativa
                                                                                                              Oryza sativa
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/mol_type="mRNA"
/db_xref="GDB:3881200"
/db_xref="taxon:9606"
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Primates;

 Mismatches

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Pred. No. 2.2e+03;
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TITLE
JOURNAL
              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Barkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Mashingtion Genome Center: Vector
Trimming: cross match from University of Mashingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Mashingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 17
contiguous PHRED high quality bases following vector sequence.
Plate: LLCM2 row: D column: 12
High quality sequence stop: 17.
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Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2819675.5prime
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
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AW247165
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA llbrary (HD)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E_coli_DH10B"
Location/Qualifiers
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Pred. No. 1e+03;
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sapiens cDNA clone IMAGE:2819675 3',
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Query Match
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CF318426/c
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.
Song,S.I., Kim,JK.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF318426
CF318426.1 GI:33690187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                       /clone lib="OSHARCI-overexpressing transgenic rice plasmid cDNA lIbrary (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B" (phage-resistant)"
/clone_lib="NIH MGC_7"
/clone_lib="NIH MGC_7"
/clone_lib="NIH MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                        /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="B.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                               /clone="HD--08-I20"
                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:4530"
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/cell_line="MGC3"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                   0.2%;
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                        Score 14.4; DB 1; Length 19; Pred. No. 1.4e+03;
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Pred. No. 1.1e+03;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bhnahm@bio.myongji.ac.kr
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SOURCE ORGANISM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0531 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg.,
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0531C04"
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1 (bases 1 to 19)

Dunn, D., Aoyggi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: H column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                  Conservative
                                                                                                                                                                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of push2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb_plasmid UUGCIM library"
/note="Vector: pwp42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20
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strain="C57BL/6J"
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                                                                                                        93.8%;
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                              4478
                                                                                                           Score 14.4; DB 1; Length 19; Pred. No. 1.4e+03;
                                                                                  Mismatches
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AZ991606
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                                                                                             Query Match
Best Local Similarity
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6741 TTCTTAAAATCTGATC 6756
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2M0275K24R Mouse 10kb plasmid
clone UUGC2M0275K24 R, genomi
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Nouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0275 row: K column: 24
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
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Fax: 801 585 7177
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                                                                       Conservative
                                                                                                                                                                    Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. coli strain XL10-Gold, T1-resistant, F-" /Clone lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="UUGC2M0275K24"
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/strain="C57BL/6J"
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                                                                                             93.8%;
                                                                                                                           0.2%;
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                                                                                                Score 14.4; DB 1;
Pred. No. 1.4e+03;
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mid UUGC2M library Mus musculus genomic
                                                                          Indels
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AZ368518/c
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                                              4464 TITTTTTTTTTTTTT 4479
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Nose whole genome scaffolding with paired end reads from 10kb
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1M0118G09R Mouse 10kb plasmid
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                                                                                                                      Similarity
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                                                                                               Conservative
                                                                                                                                                                                                                                                        musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA. and transformed into
                                                                                                                                                                                                         adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene)
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0118G09"
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                                                                                                                                                                                               selected for ampicillin resistance."
                                                                                                                      93.8%;
                                                                                                                                              0.2%;
                                                                                                                    Score 14.4; DB 1;
Pred. No. 1.5e+03;
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                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) Missouri 63134 For St. (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Eleck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max (soybean)
Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            info@genomesystems.com web site: www.genomesystems.com
                                                     GCAAGGAGGAGGAGG 2881
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                        /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erpelding."
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                                                                                                                                     0.2%;
                                                                                                                                                                                                                                                    by Dr. Randy Shoemaker and Dr.
                                                                                                        0
                                                                                                                                     Score 14.4;
Pred. No. 1.
                                                                                                                                        1.8e+03
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                          4462 ACTITITITITITIT 4477
16
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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1M0560L14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560L14 R, genomic survey sequence.
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1 (bases 1 to 22)
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801 585 7177
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                                                                                                  Conservative
                                                                                                                                                                                            Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWN42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UUGC1M0560L14"
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                                                                                                                       93.8%;
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Rodentia;
                                                                                                                          Score 14.4; DB 1;
Pred. No. 1.8e+03;
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                                                                                                                                               Length 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                           plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hc Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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AL478342.1 GI:11842152
GSS.
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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GSS.
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
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/mol_type="genomic DNA"
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/clone="193a07"
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Pred. No. 1.8e+03;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                              Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TA155F12Q 24 bp DNA linear T. brucei sheared genomic DNA clone 155f12, reverse
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High quality sequence stop: 24.
Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 11
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AL472698.1 GI:11838089
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 24)
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/strain="C57BL/6J"
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                                                                                source
                                                                                                                                                                    Contact: Robert Straussey, Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Filmming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a Xhor site followed by a run of 14 or more T residues
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1 (bases 1 to 24)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs; 2819212.5prime
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                                                                                                                      polyadenylated.

Plate: LLCM1 row: A column: 5
High quality sequence stop: 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AW248929
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                   Location/Qualifiers
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="155f12"
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/clone="IMAGE:2819212"
/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab host="0H10B (phage-resistant)"
/clone\_lib="NIH\_MGC\_7"

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CF638767

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JOURNAL COMMENT
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AUTHORS
TITLE
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KEYWORDS
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N33150/c
                        LOCUS
DEFINITION
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                                                                                                                                                                                                 4018 AGAAAAAAGAGAGAAAACAAAATG 4041
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N33150 25 bp mRNA linear EST 10-JAN-19: yy06g01.sl Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270480 3' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE
                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
High quality sequence stop: 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada Tel: 905 569 4702
Fel: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-006-UTM row: 05 column: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF638767 25 bp mRNA linear D06_G05 Filamentous Forced Diploid Ustilago maydis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST Library Creation and Analyses Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nugent, K.G., Choffe, K. and Saville, B.J.
Gene Expression during Ustilago maydis Diploid Filamentous Growth:
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Ustilago maydis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Barry J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago
1 (bases 1 to 25)
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                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of california, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                       /dev_Stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="FBD12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:5270"
cell_type="Mycelia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Ustilago maydis"
                                                                                                                                                                                                                                                           0.2%;
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                                                                                                                                                                                                                                     Score 14.4; DB 1;
Pred. No. 2.1e+03;
0; Mismatches 6;
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FEATURES

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CF317007/c
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                                                                                                                                                                                                                                                              4012 AAAATGAGAAAAAAGAGAGAGAAAAC 4035
                                                                                          CF317007
                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                        24
Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                   EST
                                                                                   CF317007.1 GI:33688768
                                                                                                                    HD--06-I14.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-I14, mRNA sequence.
                                                                                                                                                    CF317007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality Seq primer: ml3 -40 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence starts: 1 High quality sequence stops: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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N33150
N33150.1 GI:1153549
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                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                             /db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGE:270480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="Male"
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                                                                                                                                                      25 bp
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TA388E06P
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Matches 18; Conserv
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5
                                                                                                                                                                                                                         Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and
nl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                              to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T. brucei sheared genomic genomic survey sequence. AL498782
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                         Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL498782.1 GI:11874504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kyeonggi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived from rice Histone Deacetylase overexpression
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/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4530"
/clone="HD--06-I14"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2.1e+03;
0; Mismatches 6;
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AZ867155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0177 row: F column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
High quality sequence stop: 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 25)
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Similarity 75.0%;
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0177F23"
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/mol type="genomic DNA"
/strain="TREU927"
/strain="TREU927"
/db xref="taxon:5691"
/clone="388e06"
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                                                                                                                                                                                                                                                                                                                                                                              sex="Male"
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Length 25;

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Plate: 0084 row: G column: 04
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
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1M0084G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0084G04 R, genomic survey sequence.
AZ348233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AZ348233.1 GI:10427470
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Length: 10000 Std Error: 0.00
0084 row: G column: 04
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDM2 (gi]4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PW942nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
/db_xref="r==--
                                                                                                                                                                                                                                                                                                                                                                                             'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0084G04"
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Pred. No. 2.1e+03;
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                                                                                                                                    RESULT 1631
R26779/c
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AUTHORS
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KEYWORDS
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VERSION
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KEYWORDS
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                        24 AAAAAAAAAAAAAAAAAAAAAA 1
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                                                                           R26779 26 bp mRNA linear EST 24 yh44f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:132611 3' similar to gb:M85164 SERUM RESPONSE FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
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                                                      ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sativa cDNA clone 30DGS--07-G13, mRNA sequence.
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                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kyeonggi,
                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4530"
/clone="30DGS--07-G13"
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                                                                                                                                                                                                                                                                                                                         75.0%;
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Pred. No. 2.1e+03;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 14.4; DB 1
Pred. No. 2.1e+03
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AZ382581/c
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                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                         AZ382581 27 bp DNA linear GSS 02-OCT-20 1M0139120R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0139120 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 1384 Std Error: 0.00 Seq primer: Promega -21m13 High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Du
Islam, H., Longacre, S., Mahmoud, M., Meenen, E.,
                                                                                                Mus musculus
                                                                                                                                                           AZ382581.1 GI:10496281
                                                                                                                                                                               AZ382581
                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project 
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:132611"
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                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.4; DB 1;
Pred. No. 2.1e+03;
0; Mismatches 6;
                                                          Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 26;
                      Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                              Euteleostomi;
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                                                          Murinae;
                                                                                                                  SOURCE
ORGANISM
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                                                            REFERENCE
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                                                                                                                                                                                                                                                                                           RESULT 1633
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Best Local
                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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6977 AAAAACAAAACAGAATGAGGTGGG 7000
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                        TA239G06Q 29 bp 1
T. brucei sheared genomic DNA clone
                                                                                                                                                                         Trypanosoma brucei
                                                                                                                                                                                                                                                                                                              genomic survey sequence
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                      Trypanosoma.
1 (bases 1 to 29)
                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                      Trypanosoma brucei
                                                                                                                                                                                                                                                          AL481179.1 GI:11846878
                                                                                                                                                                                                                                                                                       AL481179
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Insert Length: 10000 Std Erro
Plate: 0139 row: I column: 2
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Fax: 801 585 7177
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Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CACACAGGAAACAGCTATGACC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 by range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of purified compy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.4; DB 1; Pred. No. 2.2e+03;
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± 239g06, reverse
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                                                                                                                                                                                                                                                                                                                                          sequence
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                       School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX557758 Glossina morsitans morsitans adult infected gut Gmorsitans morsitans cDNA clone Tse34e05_plc, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. bruce! sequencing at the Sanger Centre
Details of T. bruce! sequencing at the Sanger Centre
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                          Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
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Genome Biol. 4 (10), R63 (2003)
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  of the cDNA all plc reads are from
3' end.
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             /organism="Glossina morsitans
/mol_type="mRNA"
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/strain="TREU927"
                                                                                     location/Qualifiers
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_species="morsitans"
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Pred. No. 2.3e+03;
0; Mismatches 6;
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                                            morsitans"
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BX561329 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse55b10_p1c, mRNA sequence.
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All clones w
                                                                                                                                                                                                                                                                                                                                                                                                                                    Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Contact: Hall N
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Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 29)
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/clone="T8e34e06_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
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                                                                                                                                            T.brucei"
                                                                                                                                                                                         /sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse55b10_pic"
/tissue_type="adult infected gut"
/clone_Tib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                 /organism="Glossina morsitans morsitans"
/mol type="mRNA"
                                                                                                                                                           note="country: Zimbabwe;
                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 2.3e+03
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Pred. No. 2.3e+03;
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DKFZp586M1320 s1 586 (synonym: hutel) Homo sapiens cDNA clone
DKFZp586M1320, mRNA sequence.
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DKFZp566G233_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp56G233, mRNA sequence.
                                                                                                                                                                                                                                                                                               Wambutt,R., Heubner,D., Mewes,H.W., EST (Wambutt, et al.)
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Unpublished (1999)
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    Location/Qualifiers
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Mammalia; Eutheria; Primates;
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blished (1999)
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larity 75.0%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566G233"
/tlssue_type="kidney"
/dev_stage="fetal"
/lab_hoste="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: Sa
                                                                                                                           /organism="Homo gapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586M1320"
                                              /clone_lib="586 (synonym: hutel)"
/note="Vector: pSport1; Site_1: N
                                                                                /tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
0.2%;
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Score 14.4; DB 1;
Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                          Site_1: NotI; Site_2: SalI/MluI"
                                                                                                                                                                                                                                                                                                               Gassenhuber, J. and Wiemann, S.
               Length 34
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AUTHORS
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AZ513919/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0360 row: E column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0360E13F Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0360E13 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308,
                                                                                                         /clone lib="Mouse 10kb plasmid UUGCIM library"
/clone="Vector: pW042nv; Purified genomic DNA from M.
/musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWnA2 (gi[4732114]gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC1M0360E13"
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UUGC1M library Mus musculus genomic
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Query Match Best Local Similarity Matches 16; Conserv

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Score 14.2; DB 1; Pred. No. 1.5e+03; 0; Mismatches 3;

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AZ645841/c
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Query Match
Best Local Similarity
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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1M0511G04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0511G04 R, genomic survey sequence.
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Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Err
Plate: 0511 row: G column: 0
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
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                                                                                                 was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hint end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt end-sin high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWn22 (gil 4732114 | gb| AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                                                   and
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="UUGC1M0511G04"
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                                                                                   selected for
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  Score 14.2; DB 1; Length 19; Pred. No. 1.5e+03;
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                                                                                 cent E. coli XL10-Gold (Stratagene) cells
ampicillin resistance."
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AW249918
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Best Local Similarity
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Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Mashingtion Genome Center:

Trimming: cross match from University of Mashingtion Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 11

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 19 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4020 AAAAAAGAGAGAAAACAAA 4038
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Other_ESTs: 2821753.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 19)
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2821753.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821753 3',
mRNA sequence.
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TITTTTTTTGTCATCAAA 19
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Location/Qualifiers
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell line="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_libe="NIH_MGC_7"
/clone_libe="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: RCORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the following Hong in t
                                                                                                                                                                                                                                                                                                                                                 insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="small cell carcinoma"
cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                Score 14.2; DB 1
Pred. No. 1.5e+03
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Best Local Similarity
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                                                                                                                                                                 4034 ACAAAATGTTATTTTATA 4052
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84112, USA
7el: 801 585 5606
Fax: 801 585 7177
AZ357587
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Mouse, whole genome scaffolding with paired end reads from 10kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0059 row: M column: 12
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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GSS.
Mus musculus (house mouse)
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19 bp DNA linear GSS 29-SEP-200
1M0059M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059M12 R, genomic survey sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi | 4732114 | gb | AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0059M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="Male"
                                                                                                                                                                                                                                                                 0.2%;
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                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                 Score 14.2; DB 1; Length 19; Pred. No. 1.5e+03;
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19 ďď

DNA

GSS 02-OCT-2000

AZ424216/c

POCUS RESULT 1643

DEFINITION

AZ424216 19 bp DNA linear GSS 03-OCT-20 1M0203011R Mouse 10kb plasmid UUGCIM library Mus musculus genomic

GSS 03-OCT-2000

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KEYWORDS
SOURCE
ORGANISM
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Best Local
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                                               4031 AAAACAAAATGTTATTTTT 4049
19
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Mouse whole genome scaffolding with paired end reads from 10kb
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High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0099 row: C column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
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/strain="C57BL/6J"
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                                                                                                     Score 14.2; DB 1; Length 19; Pred. No. 1.5e+03; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: O column: 11
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University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Location/Qualifiers
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pws42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0203011"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                   Score 14.2; DB 1;
Pred. No. 1.5e+03;
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AZ447248/C

DEFINITION

AZ447248

19 bp DNA linear GSS 04-OCT-20 1M0244H33F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244H23 F, genomic survey sequence.

GSS 04-OCT-2000

DEFINITION

AZ962226 19 bp DNA linear GSS 27-APR-200 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0231A02 F, genomic survey sequence.

ACCESSION

RESULT 1645

AZ962226/c

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                                                    3622 GGGGTGGGGTGGGAGAGG 3640
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AZ447248.1 GI:10599044
GSS.
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Insert Length: 10000 Std Error:
Plate: 0244 row: H column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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                                                                                                       Conservative
                                                                                                                                                                                                     http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi[4732114]gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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Matches 16; Conserv
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AZ962769 19 b
ZM0231P08R Mouse 10kb plasmid
clone UUGC2M0231P08 R, genomic
AZ962769 1 GI:13833996
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Insert Length: 10000 Std Error:
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Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
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GSS.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0231A02"
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Pred. No. 1.
                                                         genomic survey sequence.
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                                                                                 bp DNA linear GSS 27-APR-2001
UUGC2M library Mus musculus genomic
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RESULT 1647
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Best Local Similarity
Warches 16; Conserve
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AZ486787
AZ486787.1
GSS.
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                                                                 AZ486787 20 bp DNA linear GSS 05-OCT-200 1M0315D23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0315D23 F, genomic survey sequence.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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                         GI:10653904
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Pred. No. 1.5e+03;
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                                                                                                                     GSS 05-OCT-2000
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m the Jackson
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Best Local Similarity
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                          CF340627 20 bp mRNA linear EST 18-AU RCL1--08-K02.gl Regenerated callus lambda phage cDNA library Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.
CF340627
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Insert Length: 10000 Std Error:
Plate: 0315 row: D column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                       CF340627.1 GI:33829609
EST.
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Fax: 801 585 7177
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert
                                                                                                                                                                                                                                                                        AAAAAAGAGAGAAAACAAA 4038
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                          was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH22 (gi|4732114|gb|AF129072:1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DN was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
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/strain="C57BL/6J"
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Pred. No. 1.6e+03;
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Best Local Similarity
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EST.
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1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                 stages of Dictyostelium discoideum Unpublished (2002)
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                            Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,I
Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 20)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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                                                                                                                                    Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                        l-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
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                                                                                                         hideko@biol.tsukuba.ac.jp.
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="RCL1--08-K02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhOI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with ShOI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on
/organism="Dictyostelium
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regenerated media"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Regenerated callus lambda phage cDNA library (RCL1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:20526682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 bp mRNA linear EST 10-MAY-2002 discoideum cDNA clone VSH730 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GreenGene Biotech Inc.; Division , MyongJi University
                                   discoideum"
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AU267884/c
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                             19
Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 20)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
                                                                                                                                                                BQ586354 20 bp mRNA linear EST 06-DEC-2002 E012395-024-013-F10-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-013-F10 5-PRIME, mRNA sequence.
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Dictyostelium discoideum
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, N
Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-298-53-4664
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                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:44689"
/clone="VSH730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="VSH730"
                                                                                                                                         GI:26115926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsukuba, Ibaraki 305-8572, Japan
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Pred. No. 1.6e+03;
0; Mismatches 3
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Pred. No. 1.6e+03;
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C53693/c
                                                                                                                                                                                                                                                                       KEYWORDS
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MEDLINE
PUBMED
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Query Match
Best Local Similarity
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Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.

Expression map of the C.elegans genome

Unpublished (1996)

Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 bp m C53693 Yuji Kohara unpublished cDNA clone yk323c3 3', mRNA sequence.
                                                 Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4:
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp
Location/Qualifiers
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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Plate: 13 row: F column: 10
Seq primer: SP6; CATACGATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTGGTTGCTCCTCCCCC
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/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                orientation:
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/clone="024-013-F10"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GABI:186521"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Beta vulgaris"
/mol_type="mRNA"
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                                                                                                         411,
                                                                                                         Japan
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Caenorhabditis
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1653
AZ759903/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 0.2%;
Local Similarity 84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6234 GCACTGTTCTTTGATTGTT 6252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0553 row: B column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weißs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ759903 20 bp DNA linear GSS 16-FEB-20 1M0553B11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0553B11 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nmalia; Eutheria
(bases 1 to 20)
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSA
                                                                                                                                                            /lab_host="B. Coli strain XL10-Gold, T1-resistant, P-"/Clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                 was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="CB1489 him-8(e1489)"
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic nur"
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/clone="yk323c3"
                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0553B11"
                                                                                                                                                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lib="Yuji Kohara unpublished cDNA"
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Pred. No. 1.6e+03;
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ORGANISM
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AZ827842
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0104 row: F column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah (
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library.
/note="Vector; PMPA2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5 kb range using preparative agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                     clone="UUGC2M0104F03"
                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center
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                                                                                                                                                                                                                                the Jackson
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Duery Match Best Local

Local

Similarity

0.2%;

Score 14.2; DB 1; Length 20; Pred. No. 1.6e+03;

1.6e+03;

밁 Ś electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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RESULT 1655
AZ835133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunnogenetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0129 row: O column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ende
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Fax: 801 585 7177
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC2M0129008"
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RESULT 1656 AZ835133/c LOCUS REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION FEATURES COMMENT KEYWORDS DEFINITION TITLE Query Match Best Local : JOURNAL Matches 5473 TTTTTTTGTAAAAAGATAA 5491 16; Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rockes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb High quality sequence stop: 20. Location/Qualifiers Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: Plate: 0129 row: O column: 08 Seq primer: CGTTGTAAAACGACGGCCAGT Contact: Robert B. Weiss University of Utah Genome University of Utah Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20) Tel: 801 585 5606 Fax: 801 585 7177 Unpublished (2000) AZ835133.1 GSS. 2M0129008F Mouse 10kb plasmid UUGCIM library Muclone UUGC2M0129008 F, genomic survey sequence. 2 TTTTTTTTAAAAAAAAA 20 Mus musculus (house mouse) AZ835133 Similarity 308, Conservative musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number USA plasmid ends of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance." Biomedical Polymers Research Bldg., 20 S. /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant,
/lab host="E. Coli strain XL10-Gold, T1-resistant,
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
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Query Match

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Similarity

84.2%; 0.2%;

Score 14.2; DB 1; Pred. No. 1.6e+03;

Length 20;

밁 Ś inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Location/Qualifiers
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Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114 |gb|AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: (
Plate: 0156 row: D column: 09
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Fax: 801 585 7177
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ853429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 21.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors.
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                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clome lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                       'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="UUGC2M0156D09"
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Pred. No. 1.8e+03;
0; Mismatches 3
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UUGC1M library Mus musculus genomic
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AZ346714/c
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Best Local S
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Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0082 row: N column: 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 21)
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1M0082N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="UUGC1M0082N05"
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Pred. No. 1.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 21)
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High quality sequence stop: 21.
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Inmert Length: 10000 Std Exror: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (St) and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC1M0165A23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:10090"
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Pred. No. 1.8e+03
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JOURNAL COMMENT
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AUTHORS
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VERSION
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LOCUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0294 row: J column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
//clone lib="Mouse 10kb plasmid UUGC1M library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC1M0294J14"
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Pred. No. 1.8
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-ham 3; Indels
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chemically-competent E. coli XL10-Gold (Stratagene) cells

## and selected for ampicillin resistance."

VERSION KEYWORDS 片 S FEATURES COMMENT REFERENCE SOURCE ACCESSION LOCUS DEFINITION RESULT 1662 AZ654730/c Matches Query Match Best Local JOURNAL TITLE AUTHORS ORGANISM source Local Similarity 5704 CTTCCTTTTCCTCTTCTCT 5722 16; Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R. AZ654730 21 bp DNA linear GSS 14 1M0529P05F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0529P05 F, genomic survey sequence. Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Err Plate: 0529 row: P column: 0 Tel: 801 585 5606 Fax: 801 585 7177 University of Utah University of Utah Unpublished (2000) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21) Mus musculus Mus musculus (house mouse) AZ654730.1 GI:11791876 Seq primer: CGTTGTAAAACGACGGCCAGT Contact: Robert B. plasmid inserts Class: plasmid ends CTTCTTTCTCCCCTTCTCT 1 308, quality sequence stop: 21. Conservative was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pulsur (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." /lab host="E. Coli strain XL10-Gold, T1-resistant, F/clone\_lib="Mouse\_10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack Biomedical Polymers Research Bldg., /mol\_type="genomic DNA" /strain="C57BL/6J" Laboratory Mouse DNA Resource sex="Male clone="UUGC1M0529P05" db\_xref="taxon:10090" organism="Mus musculus" ocation/Qualifiers 0.2%; Genome Center Weiss **0**; Score 14.2; Pred. No. 1. Std Error: 0.00 Mismatches .8e+03 DB 1; Length 21; 20 from the Jackson S 2030 GSS 14-DEC-2000 0 Gaps B-" SLC, Ę 0

Length 21;

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RESULT 1663
AZ774703/c
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0004 row: G column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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1. (bases 1 to 21)
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musculus CSTBL/60 (maile) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UUGC2M0004G14"
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Pred. No. 1.8e+03;
0; Mismatches 3;
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Insert Length: 10000 Std Error:
Plate: 0073 row: I column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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quality sequence stop: 21.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0073I12"
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Pred. No. 1.8e+03
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Tel: 801 585 5606
Fax: 801 585 7177
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Insert Length: 10000 Std Error:
Plate: 0195 row: H column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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Nouse whole genome scaffolding with paired end reads from 10kb
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University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ936997.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308,
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                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreeis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: PWD42nv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone_lib="Mouse 10kb plasmid UUGC2M library"
'note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="UUGC2M0195H01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:13795578
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    0.2%;
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Score 14.2; DB 1;
Pred. No. 1.8e+03;
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RESULT 1667
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 23)
                                                                    Mus musculus
                                                                                                         SSD
                                                                                                                       AZ984045
AZ984045.1 GI:13855272
                                                                                                                                                    AZ984045
2M0265I23F Mouse 10kb plasmid
clone UUGC2M0265I23 F, genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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CF313297.1 GI:33685058
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 Dunn, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                     Mus musculus (house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrhartoideae; Oryzeae; Oryza.
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in, Kyeonggi, Korea
82 31 330 6193
82 31 321 6355
1: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

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Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site 1: ECORI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                           derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev stage="proliferated callus on 2N6 media for 2 weeks"
lab_host="B.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4530"
/clone="HD--01-G01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                  0.2%;
 Barber, M., Beacorn, T.,
                                                                                      mouse)
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                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB Pred. No. 2e+03;
                                                                                                                                                         genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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   Duval, B.,
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                                                                                                                                                                            musculus genomic
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                                                          AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 24)
Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ399663 24 bp DNA linear GSS 03-OCT-2011M0165C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0165C10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conserv
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Insert Length: 10000 Std Error:
Plate: 0265 row: I column: 23
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Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (2000)
Contact: Robert B.
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                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                               AZ399663.1 GI:10514737
GSS.
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Location/Qualifiers
                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa
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University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Insert Length: 1000 Std Err
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Fax: 801 585 7177
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Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, India Control of Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nll@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                             to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                                                                              Details of T. brucei sequencing at the Sanger Centre at http://www.sanger.ac.uk/Projects/T_brucei/.
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref=ttaxon:4530"
/clone="NACL--03-009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
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                                               /mol_type="genomic DNA"
/strain="TREU927"
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dev_stage="proliferated callus on 2N6 media for 30 days"
lab_host="E.coli DH10B"
'clone="165h05"
                                                                                              organism="Trypanosoma brucei"
                                                                                                                                             ocation/Qualifiers
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                        xref="taxon:5691"
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Pred. No. 2.3e+03;
0; Mismatches 8
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DNA clone 165h05,
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RESULT 1672
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Best Local Similarity
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Best Local
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Glossina morsitans morsitans Glossina morsitans morsitans morsitans morsitans morsitans morsitans morsitans specifications, Insecta; Pterygota; Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                            EST.
                                                                                                                                 BX554068
                                                                                                                                                                     BX554068 Glossina morsitans morsitans adult infected gut Glossina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa
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EST.
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CF277114
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14ETL--02-I11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--02-I11, mRNA sequence.
                                                                                                                 BX554068.1 GI:33378169
                                                                                                                                                  morsitans morsitans cDNA clone Tsel3c01_plc, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonuclectides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="14ETL--02-I11"
/tissue_type="leaf"
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Pred. No. 2.3e+03;
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Pred. No. 2.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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BX557470/c
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Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
                                                                                                                                                                                                                                                                                                                                                Glossina morsitans moreitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX557470 Glossina morsitans morsitans adult infected gut morsitans morsitans cDNA clone Tse32f01_plc, mRNA sequence BX557470
BX557470.1 GI:33428655
                                                                                                                                                                                                                                           Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bangor LL57 2UW
All clones with
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Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                     response genes
Genome Biol. 4 (10), R63
                                                                                                                                                                                                                                                                                                                               Hippoboscoidea; Gl
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
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Genome Biol. 4 (10), R63 (2003)
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illarity 70.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glossina morsitans morsi
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mors
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T.brucei"
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Pred. No. 2.3e
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                                                                                                                                                                                                                                                           Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UM
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
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/clone_Tib="Glossina morsitans mo
                                                                                                    /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
                                                                                                                                      /organism="Glossina morsitans
/mol_type="mRNA"
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/tissue_type="adult infected gu
/tlone_Tib="Glossina morsitans
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/mol_type="mRNA"
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/db_xref="taxon:37546"
              note="country: Zimbabwe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for Clones, please contact: Mike Lehane
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Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                               BX551100 Glossina morsitans morsitans adult infected
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/db xref=""eaxon:37546"
/clone="Tse42e03 plc"
/clone_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
                               Contact: Hall N
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Genome Biol. 4 (10),
22881942
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Bangor LL57 2UW
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Genome Biol. 4 (10), R63 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.4%;
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                                                                                 R63
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Pred. No. 2.3e
0; Mismatches
                                                                                 (2003)
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Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina
                                                                                                                                                                                                                                                                                                                                                                                                            BX553142
33 bp mRNA linear EST 10-0
BX553142 Glossina morsitans morsitans adult infected gut Glo
morsitans morsitans cDNA Clone Tse127f01_plc, mRNA sequence
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                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for Clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Hippoboscoidea, Glossinidae, Glossina.

[ (bases 1 to 32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:37546"
/clome="Tse116601_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans mo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
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   analysis of
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AZ861400/c
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ORGANISM
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Best Local Similarity
                                                                                                                                                   source
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Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All cloner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4021 AAAAAGAGAGAAAACAAAATGTTATTT 4047
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                                                                                                                                                                   High quality sequence stop: 35.
Location/Qualifiers
                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: 0 column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 300, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 35)
1 (bases 1 to 35)
2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="Tse127f01_plc"
/tlssue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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/mol_type="mRNA"
/sub_species="morsitans"
'lab_host="E. Coli strain XL10-Gold,
                          'sex≕"Male"
                                            clone="UUGC2M0167013"
                                                                    db xref="taxon:10090"
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Pred. No. 2.3e+03;
0; Mismatches 8;
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  T1-resistant,
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                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                     Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: 0 column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Meg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ586422
14 bp mRNA linear EST 06-DEC-200: S013307-024-013-O02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-0.3-O02 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Leb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22362189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta vulgaris
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22; Conservative
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/note="Vector: PWD42nv; Purified genomic DNA fro
musculus C57BL/6J (male) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNH42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                             /db_xref="GABI:186441"
/db_xref="taxon:161934"
/clone="024-013-002"
                                                                                                                                                                                                            organism="Beta vulgaris"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                              /tissue_type="leaf"
/lab_host="EMDH10B"
clone_lib="MPIZ-ADIS-024-leaf"
                                                                                                                                                                                   cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                             (ne) "
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Pred. No. 2.2e+03
0; Mismatches 1:
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SQ13302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-B02 3-PRIME, mRNA sequence.
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Line Weg 10, 50829 Koein, Germany
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Beta vulgaris
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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                              /tissue_type="leaf"
/lab_host="RMDH10B"
/clone_lib="MMPIZ-ADIS-024-leaf"
/clone_lib="MMPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/cDNA library from sugar beet, library provided by KWS
CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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                                                                                                                                                           orientation:
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:161934"
/clone="024-009-B02"
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REFERENCE

AUTHORS

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Lota;
Lota; Magnoliophyta; eudicotyledons; core eudicots;
Lota; Magnoliophyta; eudicotyledons;
Lota; Magnoliophyta; Embryophyta;
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Lota; Magnoliophyta; Embryophyta; Embryophyta;
Lota; Magnoliophyta; Eudicotyledons; Core eudicots;
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Lota; Magnoliophyta; eudicotyledons; Eu
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S014009-024-015-I20-T7
CDNA Clone 024-015-I20
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EST.
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Max-Planck-Institute for Plant Breeding
Carl-yon-Linne Weg 10, 50829 Koeln, Gerr
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                                       TTTTTTTTTTTT 4477
TTTTTTTTTTTTT 14
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                                                                                                                                                                                                                                                                          Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="MPIZ-ADIS-024-storage root",
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/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
b.schulz@kws.de; cloning sites Sall-NotI, primer sites
                                                                                                                                                                                                                                                                                                                                                                                                                      SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;
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/lab_host="EMDH10B"
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/clone="024-015-I20"
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/mol_type="mRNA"
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Pred. No.
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Pred. No. 8.7e+02;
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                                              mRNA linear EST 06-DEC-:
CDNA clone 024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
B0590261
B0590261.1 GI:26119844
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophylales; Amaranthaceae; Beta.

1 (bases 1 to 14)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
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BQ590242.1 GI:26119825
EST.
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14 bp mRNA linear EST 06-DEC-2:
E0112840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-E16 5-PRIME, mRNA sequence.
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primer: SP6; CATACGATTTAGGTGACACTATAG.
vulgarie
vulgarie
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/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
/note="Vector: pcMVSPORT6; Site 1: Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
bischtiz@kws.de; cloning sites Sall-NotI, primer sites and
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/lab_host="EMDH10B"
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/mol_type="mRNA"
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E012715-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-H18 3-PRIME, mRNA sequence.
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Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet guarant J. 32 (5), 845-857 (2002)
                                                                         Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                Eukaryotā, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)
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Insert Length: 14 Std Error: 0.00
Plate: 19 row: K Column: 14
Seq primer: T7; GTAATACGACTCACTATAGGGC
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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1 (bases 1 to 14)
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/clone_tib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: Thrary provided by KWS
CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
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/clone="024-019-K14"
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|mol_type="mRNA"
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.0
Plate: 17 row: N column: 20
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig R Schull R Weisshaar R Hennig S Steinfath M
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                                                                                           Carl-von-Linne Weg 10, 50829 Koeln,
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
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Insert Length: 14 Std Error: 0.00
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ADIS DNA core facility at MPIZ
                                                                              Fax: 00492215062851
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/lab_host="MDH10B"
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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/mol_type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
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/clone="024-017-H18"
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                            Std Error: 0.00
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BQ591207
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                                                                                                                                                                                                                                                                                                 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                         Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 04
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lei
and Radelof,U.
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Caryophyllales; Amaranthaceae; Beta.
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Beta vulgaris
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EST.
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14 bp mRNA linear EST 06-DEC-:
E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
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Location/Qualifiers
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/note="Vector: pCMVSPORT6; Site 1: Salt; Site 2: Not1;
/note Total from sugar beet, library provided by KWS
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites al
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/db_xref="GABI:188904"
/db_xref="taxon:161934"
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Pred. No. 8.7e+(
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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1 (bases 1 to 14)
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Max-Planck-Institute for Plant Breeding Research
Carl-Yon-Line Weg 10, 50829 Koeln, Germany
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E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA Clone 024-017-B15 3-PRIME, mRNA sequence.
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Insert Length: 14 Std Error: 0.00
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Drungowaki,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J.,
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                                                                                    /tissue_type="storage root"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Beta vulgaris"
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Plate: 17 row: M column: 04
Sear primer: T7; GTAATACGACTCACTATAGGGC
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Meg 10, 50829 Koeln, Germany
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1 (bases 1 to 14)
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                                                                                    SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                           /tissue_type="storage root"
//lab host="EMDH108"
/clone lib="MPIZ-ADIS-024-storage root"
/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/cDNA library from sugar beet, library provided by KMS
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites ar
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100.0%; Pred. No. 8.7e+02;
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CF277935 14 bp mRNA linear EST 14-AUG-20 14ETL--03-K11.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza Bativa cDNA clone 14ETL--03-K11, mRNA sequence. CF277935 CF277935.1 GI:33655321
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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14 bp mRNA linear EST 06-DEC-2002
E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-028-C03 5-PRIME, mRNA sequence.
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Plate: 28 row: C column: 03
Seq primer: SP6; CATACGATTTAGGTGACACTATAG
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1 (bases 1 to 14)
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/note="Vector: pcwVsPORT6; Site 1: Sall; Site 2: Not!;
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/lab_host="EMDH10B"
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/clone="024-028-C03"
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|mol_type="mRNA"
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Ewkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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1 (bases 6 to 14)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTS Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Location/Qualifiers
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/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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/mol_type="mRNA"
/cultivar="Nackdong"
    organism="Oryza sativa"
/mol_type="mRNA"
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/clone="14ETL--03-K11"
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Pred. No. 8.7e+02;
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Fax: 82 31 321 6355
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14ETL--04-F22.91 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.
CF278452
   CF279473
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llarity 100.0%;
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="mackdong"
/db xref="taxon:4530"
/clone="14ETL--04-F22"
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with oligoribonucleotides and then used as templates for
RT-pCR."
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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/lab_host="E.coli DH10B"
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/tissue_type="leaf"
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Genomics and Genetics Institute, GreenGene Biotech Inc.; of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongji, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University Yongin, Kyeonggi, Korea
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone="148TL--05-M14"
/tissue_type="leaf"
/dev_stage="14_days_after_germination"
/lab_host="E_coli_DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 8.7e+02;
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CF281958
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Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
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                                                                        Similarity
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                             TTTTTTTTTTTT 4477
                                                          0.2%; Score 14; DB
larity 100.0%; Pred. No. 8.
Conservative 0; Mismatches
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/mol type="mcNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-D24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab host="E.coli DH108"
                                                                                                                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ETL--06-I01"
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100.0%; Pred. No.
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CF294449
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CF282350
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Best Local
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4464 TITTTTTTTTTTT 4477
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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1 (bases 1 to 14)
2 (bases 1 to 14)
2 (bases 1 to 14)
3 (bases 1 to 14)
3 (bases 1 to 14)
4 (bases 1 to 14)
4 (bases 1 to 14)
5 (bases 1 to 14)
5 (bases 1 to 14)
6 (bases 1 to 14
                    Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
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30DGS--03-P15.gl Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--03-P15, mRNA sequence.
CF294449
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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14ETL--09-N05.bl Rice etiolated leaf plasmid cDNA library (14ETL)
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Location/Qualifiers
Kyeonggi,
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="14ETL-_09-N05"
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/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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Pred. No. 8.7e+02;
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Best Local
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                              Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF295570
14 bp mRNA linear EST 14-AUG-2003
30DGS--05-J06.gl Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--05-J06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                              Similarity
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Fax: 82 31 321 6355
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                                       0.2%; Score 14; DB 1; Le llarity 100.0%; Pred. No. 8.7e+02; Conservative 0; Mismatches 0;
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Location/Qualifiers
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/tissue_type="leaf"
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/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA_was_capped
with_oligoribonucleotides_and_then_used_as_templates_for_RT-PCR."
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/lab_host="E_coli_DH10B"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was_capped_with_oligoribonucleotides_and_then_used_as_templates_for_RT-PCR."
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                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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|mol_type="mRNA"
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100.0%; Pred. No. 8.7e+02;
rative 0; Mismatches 0;
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CF297969
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Best Local Similarity
Matches 14; Conserv
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                    CF297969 14 bp mRNA linear TLEAF--01-C16.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--01-C16, mRNA sequence.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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EST.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae;
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(7LEAF) Oryza
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RESULT 1701
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                                                              Query Match 0.2%; Score 14; DB 1; Le Best Local Similarity 100.0%; Pred. No. 8.7e+02;
                                            Matches
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  4464 TTTTTTTTTTTTT 4477
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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7LEAF--01-F19.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa CDNA clone 7LEAF--01-F19, mRNA sequence.
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82 31 321 6355
                                                                                                                        /organism="Oryza sativa"
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/cultivar="Nackdong"
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/db_xref="taxon:4530"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mENA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Location/Qualifiers
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Location/Qualifiers
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/clone_Tole="Note" pcR4-TOPO; Site 1: EccRI; mRNA was capped
with_oligoribonucleotides and then used as templates for
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0; Mismatches 0;
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                                          Mismatches
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JOURNAL COMMENT
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CF299368
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Matches 14
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                                                                                                                                                                                                                                                                                    14 bp mRNA linear EST 15-AUG-2003
7LEAF--05-B01.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--05-B01, mRNA sequence.
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

1 (Dases 1 to 14)

1 (Dases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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14; Conserv
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa cDNA clone 7LEAF--03-F21, mRNA sequence.
                                                                                                                                                                                                       Oryza sativa
Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was_capped_with_oligoribonucleotides_and_then_used_as_templates_for_RT-PCR."
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and Genetics Institute, GreenGene Biotech Inc.; Division
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CF301020
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Matches 14; Conserv
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Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0;
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7LEAF--05-L10.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
CF301020
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1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale Sequencing Analysis Unpublished (2003)
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                          Conservative (
                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Mackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
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/clone_lib="Rice_leaf_plasmid_cDNA_library_II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA_was capped_with_oligoribonucleotides_and_then_used_as_templates_for_RT-pCR."
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/mol type="mrNA"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone="Nector: pCR4-TODO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
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Location/Qualifiers
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Location/Qualifiers
                                            0.2%; Score 14; DB 1; L
100.0%; Pred. No. 8.7e+02;
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1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                         Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Spermatoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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/clone_llb="Rice leaf plasmid cDNA library II (7LEAF)"
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100.0%; Pred. No. 8.7e+02;
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                                                                                  Lee, T.H., Shin, Y.C.,
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(7LEAF) Oryza
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                                     Query Match
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       14;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, Greendene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., La

Song,S.I., Kim,JK.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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TLEAF--08-G18.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
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Location/Qualifiers
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                                        Similarity
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   Conservative 0;
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                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Mackdong"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-08-GL8"
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/dev_stage="7 days after germination"
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/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECGRI; mRNA_was_capped_with_oligoribonucleotides_and_then_used_as_templates_for_pro__CT_0000; for the property of the proper
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/clone="TLEAF"--06-D16"
/clone="TLEAF"--06-D16"
/tissue_type="test"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
/note="Vector: pCR4-TOPO; Site 1: BcoRI; mRNA was capped
/note="vector: pCR4-TOPO; Site 1: BcoRI; mRNA was capped
/note="vector: pCR4-TOPO; Site 1: BcoRI; mRNA was capped
/note processed to the process of the pr
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/cultivar="Nackdong"
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100.0%; Pred. No.
                                                                          0.2%;
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Score 14; DB 1; Pred. No. 8.76
0; Mismatches
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                             DB 1; Le
. 8.7e+02;
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thes 0;
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Best Local Similarity
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                                            HITLE
                                                                                                               AUTHORS
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T..

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., 1

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTI

Unpublished (2003)
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                                                                                                                                                                          Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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CF308006.1 GI:33679767
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
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/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--08-M05"
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/dev_stage="7 days after germination"
/lab_host="E.coli DHLOBG
/lab_host="E.coli DHLOBG
/clome_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clome_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
/mth_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:33674607
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Matches 14; Conserv
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Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJin, Kyeonggi, Korea Tel: 82 31 330 6193

Fax: 82 31 321 6355
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CF308220.1 GI:33679981
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14 bp mRNA linear EST 15-AUG-2003
ABF--01-P06.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF--01-P06"
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/clone_lib="ABF3"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
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cDNA library (ABF)"
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/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
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100.0%; Pred. No. 8.7e+02;
htive 0; Mismatches 0;
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CF308918
CF308918.1 GI:33680679
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                                                              CF308918 14 bp mRNA linear ABF--02-016.bl ABF3-overexpressing transgenic rice library (ABF) Oryza sativa cDNA clone ABF--02-016,
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Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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/clome_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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/mol_type="mRNA"
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                              Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
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Tel: 82 31 330 6193
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82 31 321 6355
1: bhnahm@ggbio.com,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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organism="Oryza sativa"
'mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 1; L; Pred. No. 8.7e+02;
                                                                         bhnahm@bio.myongji.ac.kr
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Best Local Similarity
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                                                14;
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF311201 14 bp mRNA linear ABF--06-F09.gl ABF3-overexpressing transgenic rice library (ABF) Oryza sativa cDNA clone ABF--06-F09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhn
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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CF311201.1 GI:33682962
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                                                Conservative
                                                                                                                                           /tissue_type="leaf"
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cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-essponsive element binding transcription factor 3 overexpression
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nahm B.H.
                                                                                                                                line
                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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                                                             100.0%;
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Pred. No.
                                                                 Score 14;
Pred. No.
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bhnahm@bio.myongji.ac.kr
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                                                                 DB 1; Lo. 8.7e+02;
                                              0; Indels
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AUTHORS
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CF311813
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               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T.H., Shin, Song, S. I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                          HD--08-Gl3.b1 OsHDAC1-overexpressing library (HD) Oryza sativa cDNA clone CF318323 CF318323.1 GI:33690084
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                                                                                                                                                                                     Oryza sativa
Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
  Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                     CF318323
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Location/Qualifiers
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/cultivar="Nackdong"
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(DNA library (ABF)"

(note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for zhrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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100.0%; Pred. No. 8.7e+02;
ative 0; Mismatches 0;
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RESULT 1717
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AUTHORS
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JOURNAL
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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EST.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Location/Qualifiers
                                                                 /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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(DNA library (HD)"

(note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
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/clone="HD--08-J08"
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/cultivar="Nackdong"
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/mol_type="mRNA"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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/clone="HD--08-G13"
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'cultivar="Nackdong"
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100.0%; Pred. No. 8.7e+02;
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CF319826
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JOURNAL
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Best Local Similarity
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                                                          HD--12-G24.gl OsHDAC1-overexpressing transgenic rice plasmid cD library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence. CF321246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 14)
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
                   CF321246.1 GI:33693007
EST.
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  Oryza sativa
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Unpublished (2003)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="proliferated callus on 2N6 media for 2 weeks" /lab_host="E.coli DH10B" /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived from rice Histone Deacetylase overexpression
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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100.0%; Pred. No.
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Best Local S
Matches 14
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1 (bases 1 to 14)

1 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

1 Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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14 bp mRNA linear EST 18-AUG-2003

NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-H01, mRNA sequence.
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Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                       gin, Kyeonggi, Ko
: 82 31 330 6193
: 82 31 321 6355
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82 31 321 6355
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                                                                                  bhnahm@ggbio.com, bhna
Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="HD--12-G24"
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/note="Vector: pCR4-TOPO; Site 1: ECORI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
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Pred. No. 8.7e+02;
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                                                                                                        .myongji.ac.kr
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rice plasmid

Tracheophyta;

Shin, Y.C.,

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REFERENCE
AUTHORS
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CF327119
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Best Local Similarity
Matches 14; Conserv
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CF327203 14 bp mRNA linear EST NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--01-J16, mRNA sequence.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NACL--01-H14.bl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-H14, mRNA sequence. CF327119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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llarity 100.0%; Pred. No. 8.7e+02;
Conservative 0; Mismatches 0;
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Location/Qualifiers
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/clone_lib="Rice_callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for RT-pCR."
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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/mol_type="mRNA"
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cive 0; Mismatches
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CF327445
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Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeenggi, Korea Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                               Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF327445 14 bp mRNA linear EST 18-AUG-2003 NACL--01-024.bl Rice callus plasmid cDNA library (NACL) Oryza Bativa cDNA clone NACL--01-024, mRNA sequence.
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CF327203.1
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Conservative (
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Location/Qualifiers
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/organism="Oryza sativa"
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RESULT 1725
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LOCUS CF328540 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-H24.bl Rice callus plasmid cDNA library (NACL) Oryza
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/clone_ib="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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/cultivar="Nackdong"
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/clone="NACL--03-G21"
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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1 (bases 1 to 14)
1 (bases 1 to 14)
1 (Sim, J.S., Jun, K.M., Cheong, P. J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                           Email: bhnahm@ggbio.com, bhn.
Location/Qualifiers
                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                           Contact: Nahm B.H.
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100.0%; Pred. No.
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                                                                   bhnahm@bio.myongji.ac.kr
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8.7e+02;
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RESULT 1728
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AUTHORS
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CF328994
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Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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CF328994
  CF329217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 82 31 330 6193 Fax: 82 31 321 6355
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Genomics and Genetics Institute, Cof Bioscience and Bioinformatics,
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EST.
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with oligoribonucleotides and then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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, MyongJi University
  mRNA
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

LCcattion/Qualifiers

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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CF329990.1
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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with oligoribonuclectides and then used as templates for
RT-PCR."
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Pred. No. 8.7e+02;
0; Mismatches 0;
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                Similarity 100.0%;
14; Conservative (
                                         TTTTTTTTTTTT 4477
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                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
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/cultivar="mRNAckdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."
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/clone="NACL--05-I11"
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/___l +\__="mpNl"
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cultivar="Nackdong"
                                                                                0.2%; Score 14; DB 1; Length 14; L00.0%; Pred. No. 8.7e+02; Love 0; Mismatches 0; Indels
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Oryza
                                                                                  Gaps
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            NACL--08-C10.bl Rice callus plasmid cDNA linear BST 18-AUG-2003 sativa cDNA clone NACL--08-C10, mRNA sequence.
CF331861
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L.

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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NACL--07-F09.bl Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F09, mRNA sequence.
CF331272
                                     Genomics and Genetics Institute, GreenGene Biotech Inc., of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6133 Fax: 82 31 321 6355
                                                                                                                                             Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 14)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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bhnahm@ggbio.com, bhna
Location/Qualifiers
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Location/Qualifiers
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/mol type="mRNA"
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with oligoribonucleotides and then used as templates for
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                      bhnahm@bio.myongji.ac.kr
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CF333214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@cabio com
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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JMT--02-A10.bl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
CF333214
CF333214 GI:33814707
EST.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/mol type="mRNA"
/culTivar="Nackdong"
/db xref="taxon:4530"
/db xref="taxon:4530"
/clone="NACL--08-C10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--02-A10"
/tissue_type="leaf"
                                                                                                                                                                                               /dev_stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="ALJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Pred. No. 8.7e+02;
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5. 8.7e+02;
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AUTHORS
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AUTHORS
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CF333399
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatorideae; Oryzeae; Oryza.

1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                           CF333399.1
EST.
                                                                                                                                                                                                                                                                                                                                                        CF333399 14 bp mRNA linear EST 18-AUG-2003
JMT--02-E12.gl AtJMT-overexpressing transgenic rice plasmid cDNA
Library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                      library (JMT)
CF333399
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF333215

JMT--02-A10.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/clone="UMT-02-A10"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Pred. No. 8.7e+02;
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Tel: 82
Fax: 82
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kycea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.
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31 321 6355
                                                                                                                   /dev stage="14 days after germination"
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/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JWT)"
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/clone lib="AtLMM-overexpressing transgenic rice plasmid cDNA library (JMT)"
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was reverse transcribed and then used for PCR, mRNA was
pepared from Arabidopsis Jasmoinate Carboxy1
                                      methyltransferase overexpression line.
                                                            was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/mol_type="mRNA"
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100.0%; Pred. No.
  0.2%;
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  Score 14;
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thes 0;
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Length 14;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)
                                                                                                                       Oryza sativa
                                                                                                                                                            Oryza sativa
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="Nackdong"
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/clone="JMT--03-105"
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/lab_hist="E.coli DH10B"
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plasmid cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

1 (Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMT--05-J13.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence. CF335781
                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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/cultivar="Nackdong"
                                                                   tissue_type="leaf"
                                                                                         db_xref="taxon:4530"/clone="JMT--05-J13"
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/lab_host="E.coli DH10B"
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/clone="JMT--03-I11"
/tissue_type="leaf"
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Pred. No. 8.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                         bhnahm@bio.myongji.ac.kr
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CF336106 14 bp mRNA linear EST 18-AUG-2003 JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence. CF336106 CF336106.1 GI:33820590
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech In of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa
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JMT--06-A10.gl AtJMT-overexpressing transgenic rice
library (JMT) Oryza sativa cDNA clone JMT--06-A10, n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/clone="UMT--06-A10"
/tissue_type="leaf"
/dey stage="14 days after germination"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
/clone_li
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Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-
was reverse transcribed and then used for PCR.
pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methyltransferase overexpression line.
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100.0%; Pred. No. 8.7e+(
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 14; DB
%; Pred. No. 8.7
0; Mismatches
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o. 8.7e+02;
o;
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                                                                  Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                           1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 bp mRNA linear EST 18-AUG-2003
JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.
CF336287
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Fax: 82 31 321 6355
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Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
/organism="Oryza sativa"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H
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1. (bases 1 to 14)
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cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxy1
                                                                                                                                                                                           /dev stage="14 days after germination"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
/cDNA library (JMT)"
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                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--06-E15"
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                           NACL--04-K23.gl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-K23, mRNA sequence. CF329379
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongIn, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                            1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, of Bioscience and Bioinformatics,
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1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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/mol_type="mRNA"
/cullivar="Mackdong"
/db xref="taxon:4530"
/clone="30DGS--04-002"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="30 days after germination"
/lab host="5.coli DH10B"
/clome lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was cap;
with oligoribonucleotides and then used as templates i
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Pred. No.
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1e+03;
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Best Local &
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                                                                           Matches
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Best Local Similarity
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16
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                                                                                                                                                                                                                                                                                                                                                                                                 Yongin, Kyeonggi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 16)
Kim,J S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
                                                                           Conservative
                                                                                                                                                   /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was car
with oligoribonucleotides and then used as templates
RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 d
/dev_stage="proliferated callus on 2N6 media for 30 d
/lab_host="E.coli DH10B"
/clone_lib="Rice_callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was cap
with oligoribonucleotides and then used as templates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT-PCR."
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/clone="14ROOT--02-G05"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/cultivar="Nackdong"
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/clone="NACL--04-K23"
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Pred. No.
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                                                                                                                                                                     mRNA was capped as templates for
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Other ESTs: 282335.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library McC sequencing
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley McC sequencing
project Clone distribution: McC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: O contiguous
PHRED high quality bases following vector sequence. Very Low
Ouality Sequence: Trace file contained 17 contiguous distinct peaks
                                                                                                17 bp mRNA linear EST 18-AUG-2003 RCL1--04-J13.91 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--04-J13, mRNA sequence. CF339347
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Oryza sativa
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2822335.3prime NIH_MGC_7
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Plate: LLCM9 row: C column: 8.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_lTne="MGC3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 7"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ZeoRI; cDNA made by oligo-dT priming. Directionally cloned into EcRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="small cell carcinoma"
/cell_līne="MGC3"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 17;
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AL Unpublished (1999)

Other_ESTs: 2821566.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project: University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
PHRED high quality bases following vector sequence. Very Low
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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14; Conserv
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Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18)
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                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on
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/db_xref="taxon:4530"
/clone="RCL1--04-J13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Regenerated callus lambda phage cDNA library (RCL1)"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
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thes 0;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: O column: 19
                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ856873
AZ856873.1 GI:13048296
GSS.
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19 bp DNA linear GSS 21
ZM0161019F Mouse 10kb plasmid UUGC1M library Mus musculus
clone.UUGC2M0161019 F, genomic survey sequence.
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High quality sequence stop: 9.
                                                                                                                                                                     Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                      High quality sequence stop: 19.
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/clone_lib="NHH MGC_7"
/clone_lib="NHH MGC_7"
/clone_lib="NHH MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                             organism="Mus musculus"
                                                                                             Location/Qualifiers
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/tissue type="small cell carcinoma"
/cell_line="MGC3"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
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                                                                                                                                 High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Sd Error: 0.00
Plate: 0213 row: L column: 19
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
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// lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// clone lib="Mouse lokb plasmid UUGCIM library"
// note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
db_xref="taxon:10090"
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100.0%; Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF301222 20 bp mRNA linear 7LEAF--05-P21.b1 Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--05-P21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com,
                                                                                                                                                                            /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--05-P21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC3M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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100.0%; Pred. No. 1.
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        bhnahm@bio.myongji.ac.kr
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FEATURES

Query Match

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Query Match Best Local Similarity

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AZ832043/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0112 row: I column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWp42 (gi|4732114|gb|AF129072.1), a .copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PW92rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC2M0112I11"
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UUGC1M library Mus musculus genomic
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Matches 14; Conserv
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Nose whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0294 row: C column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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Unpublished (2000)
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                                                                                            Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into Chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pw042nv; purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0294C02"
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100.0%; 2
  0.2%; Score 14; DB 1; Length 21; 100.0%; Pred. No. 1.9e+03; 1ve 0; Mismatches 0; Indels
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Conservative

0,

Gaps

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Query Match Best Local Similarity

Matches

14;

Conservative

100.0%; F1

0.2%; Score 14; DB 1; L 00.0%; Pred. No. 1.9e+03; Mismatches

Length 21; Indels

<u>.</u>

Gaps

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0398 row: C column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1M0398C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0398C23 F, genomic survey sequence.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi[4732114]gb[AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="Male"
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AZ785791
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                                                                                 Query Match 0.2
Best Local Similarity 100.
Matches 14; Conservative
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    4464 TTTTTTTTTTTTT 4477
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weeiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb means the process of t
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: O column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                           / Next = main.
/ (lab host = Ne. Coli strain XIIIO-Gold, Ti-resistant, F-"
/ (clone lib "Mouse 10kb plasmid UUGCIM library"
/ note = Tvector: PMD42nv; Purified genomic DNA from M.
musculus CS7BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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was blunt end-repaired with T4 DNA polymerase and T4
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adaptored DNA was purified and size-selected for a 9.5 to
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electrophoresis. Vector DNA was prepared from a derivative
of pWM42 (gi|4732114|gb|AF129072.1), a copy-number
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chemically-competent E. coli XL10-Cold (Stratagene) cells
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| 828 15.2 0.2 20 1 US-09-920-759-82<br>829 15.2 0.2 20 1 US-09-060-299-289<br>830 15.2 0.2 20 1 US-09-402-923A-289 | 825 15.2 0.2 20 1 US-09-844-5254-45<br>826 15.2 0.2 20 1 US-09-725-265-40<br>827 15.2 0.2 20 1 US-09-725-265-41                               | 823 15.2 0.2 20 1 US-09-295-593-19<br>824 15.2 0.2 20 1 US-09-676-610B-104                                                                                                                                                                                                                                | 820 15.2 0.2 20 1 US-09-639-645A-92 821 15.2 0.2 20 1 US-09-629-645A-92 821 15.2 0.3 20 1 US-09-656-731A-85                                                                                                                                                                                                                                                                                                                                                                                | 818 15.2 0.2 20 1 US-09-657-011A-28                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 816 15.2 0.2 20 1 US-09-021-701-736<br>817 15.2 0.2 20 1 US-09-489-765A-50                                                                                                                                                                                                                                                                                                                                                                 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US-09-110-517-42                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 810 15.2 0.2 20 1 US-09-429-322-70<br>811 15.2 0.2 20 1 US-09-031-626-61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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US-08-761-704-5 | 788                                                 | 786 15.4 0.2 21 1 US-09-422-978-11139 787 15.4 0.2 21 1 US-09-422-978-11139                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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| 828 15.2 0.2 20 1 US-09-920-759-82<br>829 15.2 0.2 20 1 US-09-060-299-289<br>830 15.2 0.2 20 1 US-09-402-923A-289 | 825 15.2 0.2 20 1 US-09-844-5254-45<br>826 15.2 0.2 20 1 US-09-725-265-40<br>827 15.2 0.2 20 1 US-09-725-265-41                               | 823 15.2 0.2 20 1 US-09-295-593-19<br>824 15.2 0.2 20 1 US-09-676-610B-104                                                                                                                                                                                                                                | 820 15.2 0.2 20 1 US-09-639-645A-92 821 15.2 0.2 20 1 US-09-629-645A-92 821 15.2 0.3 20 1 US-09-656-731A-85                                                                                                                                                                                                                                                                                                                                                                                | 818 15.2 0.2 20 1 US-09-657-011A-28                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 816 15.2 0.2 20 1 US-09-021-701-736<br>817 15.2 0.2 20 1 US-09-489-765A-50                                                                                                                                                                                                                                                                                                                                                                 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US-09-110-517-42                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 810 15.2 0.2 20 1 US-09-429-322-70<br>811 15.2 0.2 20 1 US-09-031-626-61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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| 828     15.2     0.2     20     1       829     15.2     0.2     20     1       830     15.2     0.2     20     1 | 825 15.2 0.2 20 1 US-09-844-5254-45 Sequence 45 826 15.2 0.2 20 1 US-09-725-265-40 Sequence 40 827 15.2 0.2 20 1 US-09-725-265-41 Sequence 41 | 823 15.2 0.2 20 1 US-09-295-593-19 Sequence 19 824 15.2 0.2 20 1 US-09-676-610B-104 Sequence 10                                                                                                                                                                                                           | 820 15.2 0.2 20 1 US-U9-330-239-9 Sequence 92 821 15.2 0.2 20 1 US-09-625-92 Sequence 92 821 15.2 0.2 20 1 US-09-645A-92 Sequence 92                                                                                                                                                                                                                                                                                                                                                       | 818 15.2 0.2 20 1 US-09-651-014A-38 Sequence 38                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 816 15.2 0.2 20 1 US-09-021-701-736 Sequence 73<br>817 15.2 0.2 20 1 US-09-489-765A-50 Sequence 50                                                                                                                                                                                                                                                                                                                                         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US-09-110-517-42 Sequence 42                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 810 15.2 0.2 20 1 US-09-429-322-70 Sequence 70 811 15.2 0.2 20 1 US-09-031-626-61 Sequence 61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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               | 788 15.4 0.2 21 1 US-09-536-393-23 Sequence         | 786 15.4 0.2 21 1 US-09-422-978-11139 Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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Sequence 7, Appli Sequence 8, Appli Sequence 63, Appli Sequence 63, Appli Sequence 77, Appl Sequence 77, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 15, Appl Sequence 15, Appl Sequence 151, Appl Sequence 151, Appl Sequence 154, Appl Sequence 154, Appl Sequence 155, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 11, Appl Sequence 27, Appl Sequence 27, Appl Sequence 37, Appl Sequence 59, Appl Sequence 59, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 150, Appl Sequence 150, Appl Sequence 151, App Sequence 152, App Sequence 153, App Sequence 153, App Sequence 154, App Sequence 154, App Sequence 155, App Sequence 157, App Sequence 158, App Sequence 159, Appl Sequence 151, App Sequence 151, App Sequence 152, App Sequence 153, App Sequence 154, App Sequence 154, App Sequence 155, Appl Sequence 154, App Sequence 154, App Sequence 155, Appl Sequence 156, Appl Sequence 157, App Sequence 158, Appl Sequence 159, Appl Sequence 159, Appl Sequence 150, Appl Sequence 150, Appl Sequence 151, Appl Sequence 152, Appl Sequence 153, Appl Sequence 154, Appl Sequence 154, Appl Sequence 155, Appl Sequence 156, Appl Sequence 156, Appl Sequence 157, Appl Sequence 158, Appl Sequence 159, Appl Sequence 159, Appl Sequence 150, Appl	Sequence 3, Appli Sequence 237, App Sequence 3, Appli Sequence 14, Appl Sequence 9, Appli Sequence 10, Appl Sequence 103, Appl Sequence 103, Appl Sequence 114, Appl Sequence 16, Appl Sequence 17, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 115, Appl Sequence 115, Appl Sequence 115, Appl Sequence 115, Appl Sequence 116, Appl Sequence 117, Appl Sequence 118, Appl Sequence 119, Appl Sequence 119, Appl Sequence 115, Appl
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AMME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 1185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-6321
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Query Match 0.4%;
Best Local Similarity 93.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Worderfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILLING DATE: May 28, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
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US-09-081-385-112
US-08-849-949-10
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US-09-980-052-99
US-09-891-318-5
US-09-111A-15
PCT-US95-02311-3
PCT-US95-07111A-15
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                       1;
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  Indels
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Sequence 20, Appl
Sequence 20, Appl
Patent No. 5194596
Patent No. 5219739
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Sequence 112, App
Sequence 27, Appli
Sequence 11, Appl
Sequence 27, Appli
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Sequence 59, Appli
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Sequence 109, App
Sequence 5, Appli
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APPLICANT: MUKHORADON:
APPLICANT: MUKHOPACHYAY, Sunil
TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA THE TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA THE TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
FILE REFERENCE: 09924-10
CURRENT FILING DATE: 1999-05-06
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTING DATE: 1299-05-06
VUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTING DATE: 1999-05-06
PERTURE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer p41
OTHER INFORMATION: FH373
US-09-306-290-25
                                                                                                                                         ; LENGTH: 33
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-251
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                                                                                                                                                                                                         APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Winna, John D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 251
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 251, Application US/09475947A Patent No. 6472154
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                                                                                    Query Match
Best Local Similarity
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Best Local S
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                                 7405 AGCAACATCAGCAGCAGCAGCAGCAGCA 7435
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5. 6221635
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2 AGCAGCAGCAGCAGCAGCAGTAGCAGCA
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                                                                                    0.4%;
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82.1%;
                                                                  Score 26.2; D
Pred. No. 31;
0; Mismatches
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Pred. No. 23;
 32
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                                                                     Gaps
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Sequence 6, Application Patent No. 5695933; GENERAL INFORMATION:

US/08068747

APPLICANT: Schalling, Martin

RESULT 4 US-08-068-747-6

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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                             TITLE OF INVENTION: Direct Deterr
TITLE OF INVENTION: Nucleotide RA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Sm.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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STREET: Lexington
CITY: Lexington
CTATE: Massachusett
          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic"
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 28-MAY-19;
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                        ZIP: 02173
                                                                                                                                                                                                              CITY: Lexington
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FILING DATE:
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28-MAY-1993
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                          Repeats in the
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                                                                                                                                                                                                                                                                                                          Human Genome
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US-08-863-639A-30
                                                                     US-08-863-639A-30
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                                                                                                                                  TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
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Query Match
Best Local Similarity
Matches 27; Conserv
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APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM compat
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ATTORNEY/AGENT INFORMATION:
                                                                                    TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sheldon & Mak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
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Local 5-
27;
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
                                                                                                                                                                                                                                                            NAME: Joseph E. Mueth REGISTRATION NUMBER: 20, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/863,639A FILING DATE: May 28, 1997 CLASSIFICATION: 435
                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 South Lake Avenue, 9th Floor
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Caskey, C. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                     Other nucleic acid
0.3%; Score 25.8; I
93.1%; Pred. No. 30;
tive 0; Mismatches
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Pred. No. 3
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                                   DB 1;
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                                   Length 30;
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Conservative

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Gaps

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7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435

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APPLICANT: Ranum et al.

APPLICANT: Ranum et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION UNMBER: US/09/135,994A

CURRENT FILING DATE: 1998-08-18

EARLIER APPLICATION NUMBER: 60/056,170

EARLIER FILING DATE: 1997-08-19

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 4

LENGTH: 30
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US-09-684-843A-4
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; ORGANISM: Homo sapiens
US-09-135-994-4
Sequence 14, Application US/08570155
Patent No. 5962332
GENERAL INFORMATION:
APPLICANT: Singer, Robert H.
APPLICANT: Taneja, Krishan L.
                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application Patent No. 6514755
GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Query Match 0.3%;
Best Local Similarity 93.1%;
Matches 27; Conservative
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Best Local Similarity 93.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ranum et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: Regents of the University of Minnesota
CURRENT APPLICATION NUMBER: US/09/684,843A
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/056,170
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 14
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Pred. No. 30;
0; Mismatches
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Pred. No. 30;
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US-08-570-155-14
                                                                                                                                                                                                                                                                                Sequence 14, Application PC/TUS9502861
GENERAL INFORMATION:
APPLICANT: Singer, Robert H.
APPLICANT: Taneja, Krishan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399,499
FILING DATE: 07 March 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,823
FILING DATE: 17 March 1994
ATTORNEY/AGENT INFORMATION:
NAME: CLAYK, PAUL T.
NAME: CLAYK, PAUL T.
NAME: CLAYK, PAUL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 542-89
TELEX: 200154
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 225 Franklin Street
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: #1.30B
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                           ZIP: 02110-2804
                                                                                           COUNTRY:
                                                                                                               CITY: Boston
STATE: Massa
                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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l Similarity 93.1%;
27; Conservative
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                                                                                                                 Massachusetts
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nucleic acid
                                                                                                                                                    225 Franklin Street
                                                                                               U.S.A.
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                                                                                                                                                                                                                            REPEATS
BY IN SITU HYBRIDIZATION
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Pred. No. 32
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PC-DOS/MS-DOS

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US-08-068-747-7
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PCT-US95-02861-14
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.3%;
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 569593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 542-89
TELEX: 200154
INFORMATION FOR SEQ ID NO:
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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FILING DATE: 17 March 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 08 Ma
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                                                           TELEPHONE:
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                                                             617-861-6240
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0; Mismatches
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Pred. No. 3;
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Query Match
Best Local Similarity
Matches 26; Conserva
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RESULT 13
US-08-113-646A-42/c
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Patent No. 5981185
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPARTIONS 95
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/863,639A
                                                                                                                                                                                                                                                                                                                                    NAME: JOSEPH E. MUETH
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matson, Robert S. APPLICANT: Coassin, Peter J. APPLICANT: Rampal, Jang B. APPLICANT: Caskey, C. T.
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: May 28, 1997 CLASSIFICATION: 435
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STREET: 22
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                                                                                                                                                                                                                                                            TYPE:
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                                                                                   7406 GCAACATCAGCAGCAGCAGCAGCAGCAGC 7434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                              0; Mismatches
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                                                                                                                                             Score 24.2;
Pred. No. 91;
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Pred. No.
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Sequence 42, Application US/08113646A Patent No. 5578468 GENERAL INFORMATION:

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US-08-465-384-4
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TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08465384 Patent No. 5637464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cohen, Aharon S., Alexei
APPLICANT: Belenky, and Maria Vilenchik
TITLE OF INVENTION: Method of Detecting Sub-PPB Levels of
TITLE OF INVENTION: Oligonucleotides in Biological Fluids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANTCZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 0.3%; Score 23.4; Local Similarity 96.0%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/113,646A FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                     02109
                                                                                                                                                                         Boston
                                                                                                                                   Massachusetts
: USA
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                                                                                                                                                                                         3: Lappin & Kusmer
200 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                   Version #1.25
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; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-455-627-12
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US-08-455-627-12/c
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HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-465-384-4
                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 15,966
REFERENCE/DOCKET NUMBER: 15,100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANE: 415-847-0663
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08455627
Patent No. 5571677
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
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Best Local Similarity 81.8
Matches 27; Conservative
                                                                                                                                                                                 TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                     LENGTH: 30 nucleotide
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94306-2155
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                                                                                                                                         30 nucleotides
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Five Palo Alto Square,
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   89.3%;
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Pred. No. 1.1e+02;
0; Mismatches 6;
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   Score 23.2;
Pred. No. 95;
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                    DB 1;
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                  Length 30;
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Matches

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US-08-689-856-12/c
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                                                                                                                                                  Sequence 12, Application US/08787321A Patent No. 6180777 GENERAL INCORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
APPLICANT: Horn, Thomas
TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
FILE REFERENCE: (1300)-1199.002
CURRENT APPLICATION NUMBER: US/08/787,321A
CURRENT FILING DATE: 1997-01-03
EARLIER APPLICATION NUMBER: US PROV 60/009,918
EARLIER FILING DATE: 1996-01-12
NUMBER OF SEQ ID NOS: 27
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APPLICANT: Sergei
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: Convergent Synthesis of Branched and
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
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STRANDEDNESS: 81.
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Nakamura, Jackie N. REGISTRATION NUMBER: 35,9
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Pred. No. 9
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: oligonucleotide US-08-787-321-12
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US-09-061-026-26
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                                                                                                                  US-09-061-026-26
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26,
                                                        Matches
                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                    TELEFAX: 202-783-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/068

PILING DATE: 24-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 2314

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1070 783-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                              MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacobsen, Richard
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Contryphan Peptides
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                    TELEPHONE: 202-783-6037
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                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
                                                                                                                                                           TOPOLOGY:
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                           4461 GACTTTTTTTTTTTT
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6077934
                                                                      Similarity
                                                                                                                                                                                       nucleic acid
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D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                        Conservative
                                                                                                                                                             linear
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                                                                                                                              /desc = "primer"
                                                                                                                                                                       single
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                                                                    89.3%;
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Pred. No. 95;
                                                                       Score 23.2;
Pred. No. 1
                         TGTCTT 4488
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                       1.2e+02
                                                                                      DB 1;
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                                                                                   Length 33;
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                                                           Indels
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                                                        Gaps
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RESULT 20
5478746-1/c
;PACENT NO. 5478746
;PACENT NO. 5478746
;PACENT NO. 5478746
;PACENT NO. 5478746
;PACENT NO. 5478746
;PACENT NO. 5478746
;FITTLE OF INVENTION: CDNA ENCODING ATTENUATED CELL CULTURE
;ADAPTED HEPATITIS A VIRUS GENOME
;MUMBER OF SEQUENCES: 2
;CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,646
;FILING DATE: 13-SEP-1993
;PRIOR APPLICATION DATA:
APPLICATION NUMBER: 789,640
;FILING DATE: 12-NOV-1991
;APPLICATION NUMBER: 462,916
;TILING DATE: 12-NOV-1991
;APPLICATION NUMBER: 462,916
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US-09-466-138-26
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jacobsen, Richard
APPLICANT: Olivera, Baldomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-783-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/061,026
PILING DATE: US 60/068,737
PILING DATE: 24-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Contryphan Peptides NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 755 Third CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/466,138 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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755 Thirteenth Street N.W., Suite 701-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other nucleic acid
/desc = "primer"
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Pred. No. 1.2e+02;
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US-08-863-639A-94
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                                                            Matches
                                                                         Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                  TELEFAX: (626) 795-632 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH B. Mueth
20,532
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 1185
TELECOMMUNICATION INFORMATION:
TELECHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
                                                                                                                                       TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Corel WordPer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLECTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1BH COMPUTER: Windows yo
OPERATING SYSTEM: Windows yo
OPERATING SYSTEM: Windows yo
OPERATING SYSTEM: WINDOWS YOU
OPERATING SYSTEM: CARA
                                                                                                                                                                 LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 905,146
FILING DATE: 09-SEP-1986
APPLICATION NUMBER: 652,067
FILING DATE: 19-SEP-1984
APPLICATION NUMBER: 366,165
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: May 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                           7413 CAGCAGCAGCAGCAGCAGCA 7435
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                                                            Conservative
                                                                                                                                                                                                                                                 (626) 795-6321
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                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                         May 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette,
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                                                                                                                                       Other nucleic acid
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                                          100.0%; Preu....
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.50 inch, 1.44 Mb storage
                                                                         Score 23;
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Pred. No. 1.2e+02;
                                                                         DB 1;
                                                                                         Length 24;
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                                                          Indels
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                                                          Gaps
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US-08-621-914A-3

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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 29
TYPE: DNA
ORGANISM: Homo sapiens
US-10-003-998A-7
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US-10-003-998A-7/c
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                                                                                                                                                                                                                     Sequence 7, Application US/10003998A

Patent No. 6664064

GENERAL INFORMATION:

APPLICANT: Roche Diagnostics GmbH

TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR

TITLE OF INVENTION: products

FILE REFERENCE: 5438/00/EP

CURRENT APPLICATION NUMBER: US/10/003,998A

CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08621914A
Patent No. 5707807
GENERAL INFORMATION:
APPLICANT: KATO, KIKUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%;
Best Local Similarity 92.3%;
                                                      Query Match
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-7711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090 TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE II, STANTON T.
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-107-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KATO, KIKUYA
TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
TITLE OF INVENTION: ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
Local Similarity 92.3%; nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0: FILING DATE: 26-MAR-1996
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1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 base pairs
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                 0,
                                 Score 22.8; DB 1; Length 29; Pred. No. 1.1e+02;
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Pred. No. 8
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                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
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RESULT 24
US-08-173-489C-20
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US-09-244-794A-8/c
                                            RESULT 25
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Best Local (
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APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
APPLICATION NUMBER: US 07/968,436
REFERENCE/DOCKET NUMBER: US 05/18-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (attorney) (2:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT: HEPBURN, A. G.
APPLICANT: HEPBURN, A. G.
A. G.
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DESCRIPTION: third strand derived from n-myc
DESCRIPTION: sequence region in Seq ID No. 586124419
HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GE
TITLE OF INVENTION: TR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 510 EAST 73RD STREET, CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single stranded TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                        4464 TITTITTITTTTTTTTTTTTTTGTCTTG 4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4464
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                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                        0.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 246-8959
                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                        Score 22.8; DB 1
Pred. No. 1.6e+02
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                    0
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Sequence 8, Application US/09244794A Patent No. 6214553 GENERAL INFORMATION:

APPLICANT:

Szostak, Jack W. Roberts, Richard W.

APPLICANT:

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APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/244,794A
CURRENT FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR PILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
TYPE: DATE: 1998-01-14
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                                                                                              RESULT 27
US-09-247-190-8/c
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US-09-007-005-8/c
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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Translation template
US-09-244-794A-8
                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Translation template US-09-007-005-8
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.2
Sequence 8, Application US/09247190
Patent No. 6261804
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                              4460
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA-PROTEIN
                                                                                                                                                                                                                                                                                         Length 29;
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
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; OTHER INFORMATION: Translation template
US-09-247-190-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/247,190
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-21
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 86.2
                                                                                Best Local
Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007

CURRENT APPLICATION NUMBER: US/09/244,796

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1998-01-14

ETHIER APPLICATION NUMBER: 09/007,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                . Similarity
25; Conserv
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                                                                                               0.3%;
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                                                                              Score 22.6; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.6; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                    Length 29;
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                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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US-09-238-710-8/c ; Sequence 8, Application US/09238710A ; Patent No. 6518018

RESULT 29

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GENERAL INFORMATION:
APPLICANT: Robert G. Kuimelis et al.
TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
FILE REFERENCE: 50036/009002
CURRENT APPLICATION NUMBER: US/09/282,734A
CURRENT FILING DATE: 1999-03-03
EARLIER APPLICATION NUMBER: 60/080,686
EARLIER APPLICATION NUMBER: 60/080,686
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                              RESULT 31
US-09-750-401-10
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; OTHER INFORMATION: Translation template
US-09-238-710-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/238,710A
CURRENT FILING DATE: 1999-01-28
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide used US-09-282-734-3
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 29
                                                         Sequence 10, Application US/09750401 Patent No. 6635422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09282734A Patent No. 6537749
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LENGTH: 29
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Best Local Similarity
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                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
APPLICANT: Keene, Jack D.
APPLICANT: Carson, Craig C.
APPLICANT: Tenenbaum, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Pred. No. 1.1e
0; Mismatches
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Pred. No. 1.1e+02;
0; Mismatches 4
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RESULT 33
US-09-527-345-6
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US-10-003-998A-4/c
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               SOFTWARE: F.
SEQ ID NO 6
LENGTH: 26
TYPE: DNA
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PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 32
                                                                                                                                                                                                                                                                Sequence 6, Application US/09527345
Patent No. 6331413
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
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Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Method for melting curve analysis of repetitive
TITLE OF INVENTION: products
FILE REFERENCE: 5438/00/EP
CURRENT APPLICATION NUMBER: US/10/003,998A
CURRENT FILING DATE: 2001-11-14
                                                                                       PRIOR APPLICATION NUMBER: US 60/124,820 PRIOR FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                 FILE REFERENCE: 97-71
CURRENT APPLICATION NUMBER: US/09/527,345
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                      APPLICANT: Sheppard, Paul O.
APPLICANT: Adler, David A.
TITLE OF INVENTION: SECRETED
FILE REFERENCE: 97-71
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Artificial Sequence
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                                                                         FastSEQ for Windows Version 3.0
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11.1%; Pred. No. 1.7e+02;
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Pred. No. 1
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APPLICANT: Conklin, Darrell C.
APPLICANT: Blumberg, Hal
ITITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A
FILE REFERENCE: 97-63
CURRENT APPLICATION NUMBER: US/09/167,513
CURRENT FILING DATE: 1998-10-06
EARLIER APPLICATION NUMBER: US 60/061,712
EARLIER PILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 26
TYPE: DNA
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US-09-161-939A-43
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US-09-167-513-10
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; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-527-345-6
                                                                                                                                     US-09-161-939A-43
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US-09-167-513-10
                                                                 Query Match
Best Local S
Matches 23
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Best Local Similarity 88.5
23; Conservative
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Patent No. 6486299
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Genes and Proteins Predictive and Therapeutic for
TITLE OF INVENTION: Stroke, Hypertension, Diabetes, and Obesity
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Best Local Similarity 88.5
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SEQ ID NO 43
LENGTH: 26
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    FILE REFERENCE: 15966-527
CURRENT APPLICATION NUMBER: US/09/161,939A
CURRENT FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: oligo(dT)<25>V
                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                       FEATURE:
                                                                 Local Similarity nes 23; Conserv
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Pred. No. 1.2e
1; Mismatches
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Pred. No. 1.2e+02;
                                                                                Score 22; DB 1;
Pred. No. 1.2e+02;
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Patent No. 569593
GENERAL INFORMAT
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PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent-In version 3.1
SEQ ID NO 18
LENGTH: 27
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Best Local :
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APPLICANT: Brand, Joachim
TITLE OP INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
FILE REFERENCE: 024420-00008
CURRENT APPLICATION NUMBER: US/09/325,554
CURRENT FILLING DATE: 1999-06-04
                             TELEPAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                               APPLICATION NUMBER: FILING DATE: 28-MAN CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                       ZIP:
                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington
STATE: Massachusett
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22; Conserv
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N: 435
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Pred. No. 1.3e+02;
1; Mismatches 1
                                                                        MIT-6141
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US-08-341-148-2
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Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08341148 Patent No. 5610287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09268505B Patent No. 6316192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: |
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LUO, Jianhua
TITLE OF INVENTION: Method for Enrichment
TITLE OF INVENTION: through Cyclical Remov
TITLE OF INVENTION: Fragments Whose Sequer
FILE OF INVENTION INVEST: US/09/268,505B
CURRENT APPLICATION NUMBER: US/09/268,505B
CURRENT FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: oligo d(T)
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic"
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY &
                                                                                                                                                                                                                                      APPLICANT: NIKIFOROV, THEO
APPLICANT: KNAPP, MICHAEL
TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC
TITLE OF INVENTION: ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                 CITY: WASHINGTON
                                                                                                                                                                  STREET:
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4464 TTTTTTTTTTTTTTTTTTTTTTTGTCTTG 4489
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                                                                                                                              D.C
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                                                                                                                                                                E: HOWREY & SIMON
1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 base pairs
                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for Enrichment of Unique DNA Fragments
Method for Enrichment of Unique DNA Fragments
through Cyclical Removal of PCR Adapter Attached to DNA
through Cyclical Removal of PCR Adapter Two DNA Pools
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; --
Pred. No. 1.7e+02;
"dematches 2;
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Pred. No. 1.6e+02
   Version #1.25
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US-08-460-130-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 23;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/307,307
FILING DATE: 16 September 1994
APPLICATION NUMBER: 07/794,910
FILING DATE: 20 No. 5734020ember 1991
APTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: Wong
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yuan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yuan N. Wong
TITLE OF INVENTION: Proc
TITLE OF INVENTION: of INVENTION: of NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,130
FILING DATE: 2 June 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density
MEDIUM TYPE: 5 1/4" diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version
OPERATING SYSTEM: 3.20
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: J DOLLAR STREET: Lincoln Park STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Equus caballus
IMMEDIATE SOURCE:
CLONE: Biotin-T25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 639
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.
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errest: 3 Borinski Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4464 TITTTTTTTTTTTTTTTTTTGTCTT 4488
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Pred. No. 1.2e+02;
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US-08-969-813-1
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                                                                                                                       US-08-969-813-1
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Matches 23; Conservative
                                                           Matches
                                                                                        Query Match
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APPLICANT: Summerton, James E.
APPLICANT: Weller, Dwight D.
APPLICANT: Wages, John M.
TITLE OF INVENTION: Reagent and Method for Isolation
TITLE OF INVENTION: and Detection of Selected Nucleic Acid Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 783-603:
TELEX: NO. 5734020e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
creampenance: cipil
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/969,813
FILING DATE: 13-NOC-1997
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,963
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: GOTTHEY, LEEAIN
REGISTRATION NUMBER: 37,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHNE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                     TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleotide STRANDEDNESS: Single
                                                                                                                                                                                                                                           TELEFAX:
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                                                           Conservative
                                                                                                                                     linear
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                                                                                                                                                single
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                                                                        Score 21.8; DB 1
Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                           Mismatches
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                                                                                      DB 1;
                                                           2
                                                                                    Length 25;
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                                                           Indels
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                                                           Gaps
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FILE REFERENCE: 50036/009002
CURRENT APPLICATION NUMBER: US/09/282,734A
CURRENT FILING DATE: 1999-03-03
EARLIER APPLICATION NUMBER: 60/080,686
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 44
                                                     문
                                                                                     S
                                                                                                                                                                                               ; OTHER INFORMATION: Capture probe sequence US-09-282-734-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 43
US-09-282-734-23
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US-09-183-619-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 5, Application US/09183619
; Patent No. 6103474
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Robert G. Kuimelis et al.
TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09282734A Patent No. 6537749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                          Matches
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 0.0%; Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ILSLEY, DIANE D.
APPLICANT: ACH, ROBERT A.
APPLICANT: TROLL, MARK A.
TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
FILE REFERENCE: 10981619-1
CURRENT APPLICATION NUMBER: US/09/183,619
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 08/735,381
EARLIER FILING DATE: 1996-10-21
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DELLINGER, DOUG
APPLICANT: DAHM, SUEANN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                        4464 TTTTTTTTTTTTTTTTTTTTTTGTCTT 4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                          Conservative
                                                                                                                                         92.0%;
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0.0%; Pred. No. 1.2e+02;
viematches 2;
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Pred. No. 1
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                                                                                                                                   DB 1;
1.2e+02;
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                                                                                                                                                          Length 25;
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PCT-US94-14096-2

Sequence 2, Application PC/TUS9414096 GENERAL INFORMATION: APPLICANT: NIKIFOROV, THEO

NIKIFOROV, THEO KNAPP, MICHAEL

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                                                                                                                                                                                                                                                                                                                                                                             RESULT 45
US-08-621-914A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.3%;
Best Local Similarity 92.0%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08621914A Patent No. 5707807
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: KATO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 383-6610 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Equu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: AUGRBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 639-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE TITLE OF INVENTION: ANALYSIS
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US94/14096
 APPLICATION NUMBER:
                                                                                                                           ZIP: 10036-2711
                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                NEW YORK
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1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                           KIKUYA
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US/08/621,914A
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                                                                                                                                                                                                  THE AMERICAS
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Pred. No. 1.2e+02;
0; Mismatches 2
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US-08-621-914A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08621914A Patent No. 5707807
GENERAL INFORMATION:
APPLICANT: KATO, KIKUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                             TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE III, STANTON T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKST NUMBER: 7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MOLECULAR INDEXING FOR TITLE OF INVENTION: ANALYSIS NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                               TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        TELEPHONE: (212) /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LAWRENCE III, STANTON REGISTRATION NUMBER: 25,736 REFERENCE/DOCKET NUMBER: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/621,914A FILING DATE: 26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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1155 AVENUE OF THE AMERICAS
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                                                                                                unknown
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                                                                                 other nucleic acid
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               0.3%;
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PR: 7005-107-999
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Score 21.8; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 2
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Pred. No. 1.3e+02;
0; Mismatches 2
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                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSED
                              Length 26;
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Conservative

Indels

0

Gaps

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US-09-197-951-5
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US-08-873-437-2
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                                                                                                                     Sequence 5, Application US/09197951
Patent No. 6197554
GENERAL INFORMATION:
APPLICANT: LIN, SHI-LUNG
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASCESO for Windows Version 2..
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,437
FILING DATE: 12-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,832
FILING DATE: 04-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOTTHER, SCOTT R
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 4294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-638-6245
TELEPHONE: 415-638-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-638-6071
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: PE Applied Biosystems
STREET: 850 Lincoln Centre Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: O'Neill, Roger A.
APPLICANT: Chen, Jer-Kang
APPLICANT: Chiesa, Claudia
APPLICANT: Fry George
TITLE OF INVENTION: Multiplex Polynucleotide Capture
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 26 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                   TITLE OF INVENTION: Method for Generating Full-Length cDNA Library from Single Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4464 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 4488
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ADDRESSEE: David & Raymond Patent Firm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                        CHUONG, CHENG-MING
YING, SHAO-YAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                 Score 21.8; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 2;
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APELLACANT: Hammond, Angela K.

APPLICANT: Hammond, Angela K.

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTMARE: PastSEQ for Windows Version 3.0

SEQ ID NO 38

LENGTH: 26
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US-09-522-217-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nelson, Andrew J. APPLICANT: Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (626) 571-
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,951
FILING DATE: 20-No. 619754-1998
CLASSIFICATION: CUNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Raymond Y.C.
REGISTRATION NUMBER: 37,484
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 0.3%;
Local Similarity 92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
HYPOTHETICAL: NO
ANTI-SENSE: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
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CITY: Monterey Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    571-9813
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Goster, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide primer ZC7764a US-09-522-217-38
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US-09-522-217-39
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                                                                                                                                                                                                Sequence 7, Application US/09527345
Patent No. 6331413
GENERAL INFORMATION:
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Best Local Similarity
Matches 23; Conserv
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GENERAL INFORMATION:
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Patent No. 6307
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
FILE REPERENCE: 97-71
CURRENT APPLICATION NUMBER: US/09/527,345
CURRENT FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: US 60/124,820
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                        APPLICANT: Sheppard, Paul O.
APPLICANT: Adler, David A.
TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
FILE REFERENCE: 97-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 99-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC7764b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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    Mismatches

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Pred. No. 1.3e+02;
0; Mismatches 2
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Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
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US-09-593-312-2
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                                                                                                                US-09-593-312-2
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                                           Query Match
Best Local Similarity 92.0
23; Conservative
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Best Local Similarity
Matches 23; Conser
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Patent No. 6514699
                                                                                                                                                                                                   TELEPHONE: 415-638-62:
TELEFAX: 415-638-6071
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/87:
PILING DATE:
PILING DATE:
PILING DATE:
ATTOMNEY/AGENT INFORMATION:
NAME: BOTINEY, SCOET R
REGISTRATION NUMBER: 34,25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: BOU CITY: Foster City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-638-6245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fry, George
TITLE OF INVENTION: Multiplex Polynucleotide Capture
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 94404
                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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                   4464 TTTTTTTTTTTTTTTTTTTGTCTT
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850 Lincoln Centre Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Chiesa, Claudia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Neill, Roger A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                        single
                                                                    0.3%;
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                                                                                                                                                                                                                                                                         34,298
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Pred. No. 1.3e+02;
0; Mismatches 2,
                                                                     Score 21.8;
Pred. No. 1
                                                         Mismatches
25
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                            4488
                                                                     .3e+02
                                                                                    DB 1;
                                                                                   Length 26;
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                                                         Indels
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                                                         Gaps
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RESULT 53 US-09-923-246-38

Sequence 38, Application US/09923246

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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/PRIOR APPLICATION NUMBER
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US-09-923-246-39
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LENGTH: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: No. APPLICANT: Pres
APPLICANT: Spres
APPLICANT: Fost
APPLICANT: Holl
APPLICANT: Gros
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CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Oligonucleotide primer ZC7764a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presnell, Scott R.
Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnston, Janet V.
Nelson, Andrew J.
Dillon, Stacey R.
Hammond, Angela K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster, Donald C.
Holly, Richard D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09923246
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                                                                                                                           for Windows Version 3.0
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Pred. No. 1.
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US-09-658-077-1
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CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Patent No. 6627748
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Best Local Similarity
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APPLICANT:
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APPLICANT: et al.
APPLICANT: et al.
TITLE OF INVENTION: Combinatorial Fluoresence Energy Transfer Tags And
TITLE OF INVENTION: Their Applications For Multiplex Genetic Analyses
FILE REFERENCE: 0575/62238/JPW/ADM
CURRENT APPLICATION NUMBER: US/09/658,077
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: No. 6686178ak, Julia
                                                                                                                                                                                                  FILE REFERENCE: 99-16
                                                                                                                                                                                                               ARPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
RITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
                                                                                                                                                                                                                                                                                                                          APPLICANT:
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Holly, Richard D.
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Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                        Gross, Jane A.
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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APPLICANT: Johnston, Janet V.
APPLICANT: Welson, Andrew J.
APPLICANT: Welson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/60/123,547
PRIOR APPLICATION NUMBER: US/60/123,547
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/123,904
PRIOR APPLICATION NUMBER: US/60/142,013
PRIOR FILING DATE: 1999-03-11
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US-10-295-723-39
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US-08-208-486-79/c
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GENERAL INFORMATION:
APPLICANT: Ito, Junetsu
APPLICANT: Yoo, Seung-Ku
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: PRD1-C
NUMBER OF SEQUENCES: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 39 LENGTH: 26
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LENGTH: 26
                                                                                                                         Sequence 79, Application US/08208486 Patent No. 5389531
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Best Local Similarity 92.0%;
Matches 23; Conservative
                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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TYPE: DNA
ORGANISM: Artificial Sequence
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nes 23; Conserv
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                                                                                                                                                                                                                                                                                                                            Conservative
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                    METHODS TO REPLICATE DNA in vitro USING PRD1-CATALYZED DNA REPLICATION SYSTEMS
    PRD1-CATALYZED
89
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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                                                                                                            ; ORGANISM: human
US-09-475-947A-153
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-475-947A-153
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 153
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                       Sequence 153, Application US/09475947A Patent No. 6472154 GENERAL INFORMATION:
                                      Query Match
Best Local Similarity
Matches 23; Conserv
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Best Local S
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APPLICATION NUMBER: 07/869,916

FILING DATE: April 14, 1992

APPLICATION NUMBER: Japan 240525/91

FILING DATE: August 26, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janelle Faunce Raupp

REGISTRATION NUMBER: 30,485

REFERENCE/DOCKET NUMBER: #3954-A-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (602) 956-7000

TELEPHONE: (602) 956-7475
                                                                                                                                                                                                                                                                                     APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
                                                                                                                                                                                                                                                                        FILE REFERENCE: UTSD0667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (602) 495-947:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
COMPUTER: Packard Bell (1MM PC/AT compatible)
OPERATING SYSTEM: MS-DOS, Version 5.0
SOFTWARE: WordPerfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,486
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ADDRESSEE: Cahill, S
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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155 Park One, 2141 E. Highland Ave.
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                                        Conservative
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                                                       0.3%;
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                                                        Score 21.8;
Pred. No. 1.
                                          Mismatches
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RESULT 61
US-08-870-730-9/c
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US-08-433-505-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 23; Conserval
                                                                                                                                                                                                                      Sequence 9, Application US/08870730 Patent No. 6017707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/8/433,505
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36349
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MANDRAN
APPLICANT: CROS, P
APPLICANT: DELAIR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 9, Application US/08433505
Patent No. 5695936
                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-836-2787 INFORMATION FOR SEQ ID NO:
               APPLICANT: CROS, Philippe
APPLICANT: DELAIR, Thierry
APPLICANT: CHARLES, Marie-Helene
APPLICANT: EROUT, Marie-No. 601770711e
APPLICANT: PICHOR, Christian
TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
TITLE OF INVENTION: A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EROUT, Marie-No. 569593611e
APPLICANT: PICHOT, Christian
APPLICANT: TONNELLIER, Jean-Claude
TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
TITLE OF INVENTION: A NUCLECTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
                                                                                                                                                                           APPLICANT: MANDRAND, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
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CHARLES, Marie-Helene
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llarity 92.0%;
Conservative
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ADDRESS
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Pred. No. 1.8e+02;
0; Mismatches 2;
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APPLICANT: Orum, Hendrik
APPLICANT: Seeger, Corina
FITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
FITLE OF INVENTION: Acids
FILE REPERENCE: Sequence listing
CURRENT APPLICATION NUMBER: US/09/083,123
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: EP 95118600.6
EARLIER FILING DATE: 1995-11-25
EARLIER APPLICATION NUMBER: POT/EP96/05149
EARLIER FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 8
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 30
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                                                                                                                                   US-09-083-123-3
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Best Local S
Matches 23
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                                                               Query Match
Best Local Similarity
Matches 23; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-836-6400
                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: made by humans
                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/870,730 FILING DATE: 06-JUN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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STREET: P.O. Box 19928
-CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lin
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23; Conserv
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                                                               Conservative
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Pred. No. 1.8e+02
0; Mismatches
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Pred. No. 1
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25
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                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-083-123-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08882649A Patent No. 6344316 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09083123 Patent No. 6326143
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Orum, Hendrik
APPLICANT: Seeger, Corina
TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
TITLE OF INVENTION: Acids
TITLE OF INVENTION: Acids
FILE REFERENCE: sequence listing
CURRENT APPLICATION NUMBER: US/09/083,123
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: EP 95118600.6
EARLIER FILING DATE: 1995-11-25
EARLIER APPLICATION NUMBER: PCT/EP96/05149
EARLIER FILING DATE: 1996-11-22
VINIONES OF TO NOC. 0
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,649A
FILING DATE: 25-Jun-1997
CLASSIFICATION: 435-006.000
PRIOR APPLICATION UNMER: US 60/010,471
FILING DATE: 23-JAN-1996
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4464 TTTTTTTTTTTTTTTTTTTTTGTCTT 4488
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                                                                                                                                                                                                                                                                                                  ADDRESSEE: Joe Liebeschuetz
STREET: Two Embarcadero Center,
                                                                                                                                                                                                                                                                                  CITY: San Francisco
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Cronin, Maureen T.
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Pred. No. 1
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                                                                                                                                 Version #1.30
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                                                                                                                        , OTHER INFORMATION: n at position 10 can be US-09-648-040-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-882-649A-10
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Robert G. Kuimelis
TITLE OF INVENTION: METHODS FOR CODING AND SORTING
TITLE OF INVENTION: TRANSLATED PROTEINS
FILE REFERENCE: 50036/032002
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/648,040
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,261
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                           Best
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                                                                                           Query Match
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                                                                                                                                                  OTHER INFORMATION: Encoding molecule NAME/KBY: misc_feature LOCATION: 10
                                                                                                                                                                                                     LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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                                                                           Local
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/035,170
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: PCT/US97/01603
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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                                                                           Similarity
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-019410US
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ilarity 82.8%;
Conservative (
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Pred. No. 1.
                                                                            Score 21.6;
Pred. No. 1.
                                                               Mismatches
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                                                               Gaps
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RESULT 66 US-09-475-947A-134

Sequence 134, Application US/09475947A Patent No. 6472154 GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

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US-08-910-632-5/c
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US-09-721-154-4
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; ORGANISM: human
US-09-475-947A-134
Sequence 5, Application US/08910632B
Patent No. 6077668
GENERAL INFORMATION:
APPLICANT: KOOL, ERIC T.
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER APPLICATION NUMBER: 08/805,631
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Best Local Similarity
Matches 22; Conserv
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LENGTH: 24
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SEQ ID NO 134
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 665100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Database system including computer code TITLE OF INVENTION: for predictive cellular bioinformatics FILE REFERENCE: CytoPo07C2 CURRENT APPLICATION NUMBER: US/09/721,154 CURRENT FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: 09/311,996 PRIOR APPLICATION NUMBER: 09/311,996 PRIOR FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 14 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vaisberg, Eugeni
APPLICANT: Adams, Cynthia
APPLICANT: Sabry, James
APPLICANT: Crompton, Anne
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CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 95.
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Pred. No. 1.3e+02;
0; Mismatches 1;
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Pred. No. 1.3e+02;
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; OTHER INFORMATION: synthetic AS83 DNA nanocircle US-08-910-632-5
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                                                        Query Match
Best Local S
Matches 23
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Patent NO. 6096880
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTI
TITLE OF INVENTION: CIRCULAR DNA
TITLE OF INVENTION: DNA
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
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NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UPILING DATE: 26-FEB-9CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minneapola
                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                             STRANDEDNESS: sing TOPOLOGY: circular
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                       4464
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Similarity 88.5%;
23; Conservative
26 base pairs
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                                                                                                                                           DNA (genomic)
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                                                      Score 21.2; D
Pred. No. 1.7e
0; Mismatches
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Pred. No. 1.7e+02;
                                                                        .7e+02
                                                                                          DB 1;
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RESULT 70
US-09-569-344-5/c
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Patent No. 6368802
GENERAL INFORMATION:
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 152, Application US/09304232 Patent No. 6525185
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 23; Conserv
                APPLICANT: Fan, Jian Bing
APPLICANT: Chakrawarti, Aravinda
APPLICANT: Halushka, Marc Kenneth
APPLICANT: Case Western Reserve University School of Medicine
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Polymorphisms Associated With
TITLE OF INVENTION: Hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US 08/805,631

FILING DATE: 26-FEB-97

APPLICATION NUMBER: US 08/393,439

FILING DATE: 23-FEB-1995

APPLICATION NUMBER: US 08/047,860

APPLICATION NUMBER: US 08/047,860

FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE,DOCKET NUMBER: 220.00010140

TELEPHONE: 612-305-1226

TELEPHONE: 612-305-1226
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/569,344 FILING DATE: 11-May-2000 CLASSIFICATION: <Unknown>
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Pred. No. 1.7e+02;
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PCT-US92-10792-1
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SEQ ID NO 152
LENGTH: 29
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Matches 23; Conserv
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CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: US 60/084,641
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 909
                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/826,934
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 018547-034210US
                                                                                                                                             TELEFAX: (415) 859-3880
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: APOA4 3058
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                                 MOLECULE TYPE:
HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Triple Helix Formation at TITLE OF INVENTION: (PUNPYN) - (PUNPYN) Tracts NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                     NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-4550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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                                                                                                                             TYPE: NUCLEIC ACID
                                                                                          TOPOLOGY:
                                                                                                         STRANDEDNESS:
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               INDIVIDUAL ISOLATE: OLIGONUCLEOTIDE I, FIGURE
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333 Ravenswood Avenue
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                                                                    DNA (genomic)
                                                                                                           single
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Pred. No. 2.1e+02
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RESULT 74
US-08-863-639A-28
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US-08-267-803B-66/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Orr, Harry ...
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis

TITLE OF INVENTION: B5
                                                                                  Sequence 28, Application US/08863639A Patent No. 5981185
              GENERAL INFORMATION:
APPLICANT: Matson,
APPLICANT: Coassin
APPLICANT: Rampal,
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55458-1415
COMPUTER READRALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3%;
Best Local Similarity 88.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: F.C. CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                   h 0.3%; Score 21;
Similarity 100.0%; Pred. No.
21; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Mueting, Raasch, Gebhardt & Schwappach, P.A.
P.O. Box 581415
Matson, Robert S. Coassin, Peter J. Rampal, Jang B. Caskey, C. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Pred. No. 2.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                      1.1e+02;
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                                                                                                                                                                                                                                                                                   Length 21;
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RESULT 75
US-08-863-639A-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/08863639A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Cassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM compatib
                                                                                                 SOFTWARE: Corel WordPe
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         STREET: 225
STREET: 225
CITY: Pasadena
CTNTE: CA
TTSA
                                                                                                                                                                                                                                                                                        ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 24_
CTTY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                     STATE: C
                                                 APPLICATION NUMBER: US/08/863,639A FILING DATE: May 28, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                         ZIP:
                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: May 28 CLASSIFICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7413 CAGCAGCAGCAGCAGCAGCAG 7433
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                                                                                                                                                      IBM compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          May 28, 1997
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 20,532
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                                                                                                                                                                      3.50 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 1;
; Pred. No. 1.1e+0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1e+02;
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                                                                                                                                 US-08-863-639A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60, Application US/08863639A Patent No. 5981185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11859-1
TELEOPHONE: (626) 796-4000
TELEPAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                 TELEFAX: (626) 795-632
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: MAY 28, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                TOPOLOGY: li
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLECTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.3%; Score 21; DB 1; Length 21; Local Similarity 100.0%; Pred. No. 1.1e+02; nes 21; Conservative n. wire
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                               7413 CAGCAGCAGCAGCAGCAG 7433
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                                                                                                                                                                                                                 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                  (626) 795-6321
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM compatible
                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheldon & Mak
                                                                                                                                                Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                 single
                                                                                0.3%; Score 21;
100.0%; Pred. No.
                                                              0
                                                                Mismatches
                                                                                               DB 1;
                                                                                  1.1e+02;
                                                                                               Length 21;
                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Best Local Simer Programme 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66, Application US/08863639A Patent No. 5981185
                                                                                                                                                                                                                                                                                    Sequence 69, Appraise No. 5981185
                                                                                                                                                                                                                                                                        Patent No. 5981185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (626) 795-632
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
20,532
REGISTRATION UNMER: 20,532
REFERENCE/DOCKET NUMBER: 1185
TELECOMMUNICATION: 10F0RMATION:
TELEPHONE: (626) 795-6321
TELEFAX: (626) 795-6321
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Wordberfect 8 version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
                                                                                                                          NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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STREET: 222
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                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                            Application US/08863639A
                                                                                                            225 South Lake Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: Sheldon & Mak
225 South Lake Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.3%; Score 21;
100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                              9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1e+02
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SOPTWARE: Corel WordPerfect 8 version CURRENT APPLICATION DATA:

OPERATING SYSTEM:

IBM compatible SYSTEM: Windows 95

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RESULT 79
US-08-863-639A-87/c
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APPLICANT: Matson, Robert S.

APPLICANT: Coassin, Peter J.

APPLICANT: Cassey, C. T.

APPLICANT: Cassey, C. T.

TITLE OF INVENTION: OLICONUCLEOTIDE REPEAT ARRAYS

TITLE OF SECOUENCES: 95
                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECHNUR: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application US/08863639A
Patent No. 5981185
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FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1056-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                  TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sheldon & Mak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                               STRANDEDNESS:
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                                                  nucleic acid
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Other nucleic acid
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100.0%; Pred. No. 1.1e+02;
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US-08-400-275-13
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                                                                                                                         Matches
                                                                                                                                                       Query Match
Best Local :
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,681
FILING DATE:
APPLICATION NUMBER: US 07/613,160
APPLICATION NUMBER: US 07/613,160
APPLICATION NUMBER: US 07/613,160
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APPL
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Creason, Gary L
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 York
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                   Local Similarity
                                                       4463 CITITI
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                                                                                                                         21;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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RECOMBINANT DAM MOLECULES ENCODING PUTRESCINE
N-METHYLITRANSFERASE, AND TRANSGENIC TOBACCO PLANTS WITH
ALTERED NICOTINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                       TTTTT 4483
                                                                                                                                                   Score 21; DB 1; Pred. No. 2.3e+
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                                                                                                                      Mismatches
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RESULT 81 US-08-227-476-5/c

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                                                    ; TYPE: DNA
; ORGANISM: human
US-09-475-947A-332
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                                                                                                FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 332
LENCTH: 30
                                                                                                                                                                                                                                                                                                          Sequence 332, Application US/09475947A
Patent No. 6472154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
Query Match
Best Local Similarity
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                                                                                                                                                                                                                       APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Miller
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 40.
STREET: 40.
CITY: San Diego
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 699-3604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray, Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weseman, James C.
REGISTRATION NUMBER: 30,507
REFERENCE/DOCKET NUMBER: P0023US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       4463 CITTITITITITITITIT 4483
                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Gray, Cary, Ames & Frye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, Jeffrey E.

VENTION: METHODS AND COMPOSITIONS FOR CDNA

VENTION: SYNTHESIS
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100.0%; Pred. No.
0.3%;
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Score 21; DB 1; Length 30; Pred. No. 2.5e+02;
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hes 0;
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RESULT 84
US-09-619-103-14/c
; Sequence 14, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
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US-08-522-623-14
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                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (708) 937-9556
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,623
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/863,553
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF TITLE OF INVENTION: NUCLBIC ACID OR ANALYTE USING TOTAL INTERNAL REFLECTION NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Abbott Park
STATE: Illinois
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                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 32
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                              4463 CTTTTTTTT
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                                                                                                                                                                                      Similarity
                                                                                                                  Application US/08522623
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One Abbott Park Road
                                                                                                                                                                                                                                                                                                                                              32 base pairs
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                       0.3%; Score 21;
100.0%; Pred. No.
Live 0; Mismatcl
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                                                                                                                                                                                       2.9e+02;
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                                                                                                                                                                                                   Length 32;
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/863,553
RILING DATE: 06 APRIL 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5158.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
TELEPHONE: (708) 937-2623
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 DASE pairs
TYPE: NUCLEIC ACID
STRANDEENNESS: single
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PCT-US93-03256-14
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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: designed sequence to act as a linker
US-09-619-103-14
PCT-US93-03256-14
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SEQ ID NO 14
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin and WordPerfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03256 FILING DATE: 19930506 CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Applicat
GENERAL INFORMATION:
APPLICANT: Abbott
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TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
FRIOR APPLICATION NUMBER: 60/145,834
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                        FEATURE:
                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF TOTAL INTERNAL REFLECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Abbott Laboratories STREET: One Abbott Park Road CITY: Abbott Park
                NAME/KEY: misc_feature LOCATION: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4464 TTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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; Pred. No.
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2.9e+02
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                                                                                                                          RESULT 87
US-08-486-421-50/c
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                                                                                                                                                                                                                                                                                                                        US-08-014-943A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPAX: 212 869-8864/9741
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
                                                                                           Sequence 50, Application US/08486421 Patent No. 5672479
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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                                                                              GENERAL INFORMATION:
                            APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 02) FEB CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                             4464 TITTTTTTTTTTTTTTTTTTTTGTCT 4487
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1155 Avenue of the
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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00.0%; Pred. No.
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Loning And Expression Of PUR Protein
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                        Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                     Length 24;
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ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas

New York

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RESULT 88
US-08-470-911-50/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5756684
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/08470911 Patent No. 5756684
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Best Local
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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                                                                                                                                                                                                                                                                                  ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-UN-1995
CIASCIPICATION TO APPLICATION TO A
                           NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 69:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 A
CITY: New York
STATE: New Yor
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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Y: U.S.A.
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(212) 869-9741/8864
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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; MOLECULE TYPE: US-08-470-911-50
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US-08-735-381-1/c
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Patent No. 5853993
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Best Local Similarity
Matches 22; Conserv
                               Matches
                                                             Query Match
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                                                                                                                                                                                                                                TELEX: 348-461
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/735,381
FILING DATE: 21-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                      MOLECULE TYPE: MRN
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
                                                                                                      HYPOTHETICAL:
ANTI-SENSE: 1
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                                                                                                                                                                                                                                TELEFAX: 50.
TELEFAX: 348-461
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TELEPHONE: 650-852-8063
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ZIP: 94304-1126
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hewlett-Packard Company, Legal Dept., ADDRESSEE: Intellectual Property STREET: 1501 Page Mill Road, MS 4U-10
                                             Local
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                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                 TYPE: nucleic acid
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                                             Similarity
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llarity 91.7%;
Conservative
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Pred. No. 1.
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                               Score 20.8; DB 1, Pred. No. 1.7e+02, 0; Mismatches
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                                                            Length 24;
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APPLICANT: DELINGER, DOUGLAS J.
APPLICANT: DAHM, SUEANN C.
APPLICANT: ILSLEY, DIANE D.
APPLICANT: APPLICANT: TROLL, MARK A.
APPLICANT: TROLL, MARK A.
TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT FILE REFERENCE: 10981619-1
CURRENT APPLICATION NUMBER: US/09/183,619
CURRENT APPLICATION NUMBER: 08/735,381
EARLIER APPLICATION NUMBER: 08/735,381
EARLIER FILING DATE: 1996-10-21
NUMBER OF SEQ ID NOS: 7
SOFTMARE: Patentin Ver. 2.0
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,809

PILING DATE: 07-UN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/470,911

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LANZA A.

REGISTRATION NUMBER: 30,742

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Patent No. 6103474
GENERAL INFORMATION:
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Best Local (
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 692: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9990 TELEFAX: (212) 869-9741/8864
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APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 24 base pairs
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22; Conserv
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Y: U.S.A.
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1155 Avenue of the Americas
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Query Match
Best Local Similarity
Matches 22; Conserv
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Patent No. 6110682
GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
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LENGTH: 24
TYPE: RNA
ORGANISM: Artificial Sequence
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Matches :
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TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,674
FILING DATE: 30-No. 6110682-1998
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/735,381 FILING DATE: 21-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                  HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                             LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1501 Page Mill Road, MS 4U-10
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    Conservative
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                    0.3%;
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91.7%; Pred. No. 1.7e+02;
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    0; Mismatches
                    Score 20.8; DB 1;
Pred. No. 1.7e+02;
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                                        DB 1;
                                      Length 24;
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    Indels
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  Gaps
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4464 TTTTTTTTTTTTTTTTTTTTTGTCT 4487

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RESULT 95
US-09-333-237-4/c
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US-09-025-639-4/c
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US-09-536-936-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kurn, Nurith
APPLICANT: Patel, Rajesh D.
TITLE OF INVENTION: Quantitative Determination of Nucleic
TITLE OF INVENTION: Acid Amplification Products
FILE REFERENCE: BEH-7408
CURRENT APPLICATION NUMBER: US/09/025,639
CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Matches
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CURRENT APPLICATION NUMBER: US/09/536,936
CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 24
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Patent No. 6346384
GENERAL INFORMATION:
APPLICANT: Pollner, Reinhold
TITLE OF INVENTION: Real Time Monitoring of PCR Using LOCI
GENERAL INFORMATION:
APPLICANT: Singh, Sharat
APPLICANT: Ullman, Edwin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09025639 Patent No. 6365346 GENERAL INFORMATION:
                                                     Sequence 4, Application US/09333237 Patent No. 6406667
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Best Local Similarity
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding
LOCATION: (1)...(24)
OTHER INFORMATION: Synthetic DNA Probe
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Local Similarity 91.7%;
hes 22; Conservative
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Pred. No. 1.7e+02;
0; Mismatches 2
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US-09-732-067-1/c
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RESULT 97
US-10-043-415-4/c
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                                                                                                                                                                                                                             US-09-732-067-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chemiluminescent Compositions For Use TITLE OF INVENTION: Detection Of Multiple Analytes FILE REFERENCE: BEH-7383A CURRENT APPLICATION NUMBER: US/09/333,237 CURRENT FILING DATE: 1999-06-15 PRIOR APPLICATION NUMBER: 09/025,624 PRIOR APPLICATION NUMBER: 09/025,624 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
LENGTH: 24
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
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Patent No. 645742
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APPLICANT: Singh, Rajendra
APPLICANT: DeKeczer, Steve
APPLICANT: Davalian, Dariush
TITLE OF INVENTION: Amplified Luminescent Homogeneous
TITLE OF INVENTION: Immunoassay
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/732,067
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: BEH-7385
                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: hybridization oligo
                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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91.7%; Pred. No. 1.7e+02
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Pred. No. 1.7e+02;
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                                                                                                                                                                                        DB 1;
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GENERAL INFORMATION:

APPLICANT: Kurn, Nurith

APPLICANT: Patel, Rajesh D.

TITLE OF INVENTION: Quantitative Determination of N

TITLE OF INVENTION: Acid Amplification Products

FILE REFERENCE: BEH-7408

CURRENT APPLICATION NUMBER: US/10/043,415

CURRENT FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US/99/025,639

PRIOR FILING DATE: 1998-02-18

of Nucleic

Sequence 4, Application US/10043415 Patent No. 6573054

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TITLE OF INVENTION: Database system including computer code
TITLE OF INVENTION: for predictive cellular bioinformatics
FILE REFERENCE: CytoPOO7C2
CURRENT APPLICATION NUMBER: US/09/721,154
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 09/311,996
PRIOR PILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 24
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Su, Xing
APPLICANT: Dong, Helin
APPLICANT: Dong, Helin
APPLICANT: Dong, Helin
APPLICANT: Dong, Helin
APPLICANT: Pidenas B.
TITLE OF INVENTION: Amplification of Nucleic Aci
FILE REFERENCE: 3234.2
CURRENT APPLICATION NUMBER: US/09/854,317
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 24
TYDE: DNA
ORGANISM: artificial sequence
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US-09-721-154-1
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US-09-854-317-1/c
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; OTHER INFORMATION: synthetic oligonucleotide
US-09-854-317-1
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Patent No. 6651008
GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 22; Conservative
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Best Local Similarity 91.7%;
Matches 22; Conservative
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 24
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                                                                                                                                                                                                                                              APPLICANT: Vaisberg, Eugeni
APPLICANT: Adams, Cynthia
APPLICANT: Sabry, James
APPLICANT: Crompton, Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc binding
LOCATION: (1)...(24)
OTHER INFORMATION: Synthetic DNA Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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Pred. No. 1.7e+02;
0; Mismatches 2;
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Pred. No. 1.
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.1.7e+02;
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US-08-784-208-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Spinella, Dominic G.
APPLICANT: Sajjadi, Fereydoun G.
APPLICANT: Sajjadi, METHOD FOR AN
TITLE OF INVENTION: METHOD FOR AN
TITLE OF INVENTION: OF GENES
NUMBER OF SEQUENCES: 6
                                                                    Matches
                                                                                Query Match 0.3%;
Best Local Similarity 78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.3%;
Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 22;
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,208
FILING DATE: January 15, 1997
CLASSIFICATION : 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/167
                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                   TELEPHONE:
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                   4465 TITTITTITTTTTTTTTTTTTTTGTCTTGAGACATG 4496
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 TTTTTTTTTTTTTTTTCGCCGGCGCATG
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                                                                                                                                                                                                                                                                     (213) 955-0440
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                                                                    Conservative
                                                                                                                                               ss: single
linear
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METHOD FOR ANALYZING
QUANTITATIVE EXPRESSION
OF GENES
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                                                                Score 20.8; D
Pred. No. 3.1e
0; Mismatches
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Pred. No. 1.7e+02
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                                                                                3.1e+02;
                                                                                                   DB 1;
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32
                                                                                               Length 32;
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RESULT 101 US-08-123-449A-19/c

Sequence 19,

Application US/08123449A

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US-08-458-050-19/c
; Sequence 19, Application US/08458050; Patent No. 5677289; GENERAL INFORMATION:
                                                                                                  RESULT 102
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                                                                                                                                                                                                                                                                                  US-08-123-449A-19
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
APPLICATION 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pedrick, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 714-760-040
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: NAME OF THE SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: NIH034.001QPC TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES TITLE OF INVENTION: OF RNA
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: A is linked by 2',5'-linkage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                              NAME/KEY: miscellaneous feature LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fedrick, Michael r. REGISTRATION NUMBER: 36,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                               95.5%;
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                                                                                                                                                                                                                             Score 20.4; DB 1;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                              Length 22;
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RESULT 103 US-08-847-844A-94/c

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Sequence 94, Application US/08847844A Patent No. 6150160

GENERAL INFORMATION: APPLICANT: KAZAZI

APPLICANT:

BOEKE, JEF D. MORAN, JOHN V.

KAZAZIAN JR., HAIG H.

DOMBROSKI, BETH A.

APPLICANT:

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                                                                                                                            US-08-458-050-19
                                                               Matches
                                                                                        Query Match
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TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/123,449

FILING DATE: 17-SEP-1993

APPLICATION NUMBER: PCT/US93/101-

FILING DATE: 10-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: FEGICK, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson and
STREET: 620 Newport Center Drive
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: RATAN, MAITRA
APPLICANT: KRYSTYNA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
TITLE OF INVENTION: OF RNA
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSeq Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.ZIP: 92660
                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                        OTHER INFORMATION: A is linked by 2',5'-linkage
                                                                                                                                                                                                                                       NAME/KEY: miscellaneous feature LOCATION: 1-4
                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                           LOCATION:
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                   4464 TITITITITITITITITITITGT 4485
22 TTTTTTTTTTTTTTTTTTTT
                                                                              Similarity
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                          miscellaneous feature
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                                                                              95.5%;
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                                                                                                                                           A is linked at 2' end to following base through a linker moiety
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                                                               0
                                                               Score 20.4; D
Pred. No. 1.7e
0; Mismatches
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                                                                            .7e+02:
                                                                                             DB 1; Length 22
                                                                  Indels
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RESULT 104
US-08-950-196-19/c
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                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08950196 Patent No. 6271369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICAL DATE: 16-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/006,831
PILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 215-567-202
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                        ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                           APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
APPLICANT: RATAN, MAITAR
APPLICANT: KRYSTYNA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
TITLE OF INVENTION: OF RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 215-567-2020
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 08/749,805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,844A
FILING DATE: 28-APR-1997
                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 9596-23U2
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS version
                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                      COUNTRY:
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                                                                                                                        Newport Beach
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                                                                                                                                           E: Knobbe, Martens, Olson and Bear 620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET,
                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                   Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94:
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US-09-720-201A-25/c
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                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 25
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KOHARA, MICHINORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09720201A Patent No. 6524853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                         APPLICANT: KOHARA, KYOKO
APPLICANT: TAIRA, KAZUNARI
APPLICANT: MATSUZAKI, JUNICHI
APPLICANT: MATSUZAKI, JUNICHI
APPLICANT: OHMORI, HIROSHI
TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND
TITLE OF INVENTION: ITS USE
FILE REFERENCE: 04853.0051-0000
CURRENT APPLICATION NUMBER: US/09/720,201A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: D98/177,820
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: PCT/JP99/03381
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US93/
FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIHC
                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: (HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE:
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TELEPHONE: 714-760-0404
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APPLICATION NUMBER: 1
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: A is linked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: miscellaneous feature LOCATION: 1-4
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STRANDEDNESS: sing
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; OTHER INFORMATION: Description of Artificial Sequence: Poly A ; OTHER INFORMATION: nucleotide sequence US-09-720-201A-25
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Patent No. 6651008
GENERAL INFORMATION:
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LENGTH: 24
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 09/311,996
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vaisberg, Eugeni
APPLICANT: Adams, Cynthia
APPLICANT: Sabry, James
APPLICANT: Crompton, Anne
TITLE OF INVENTION: for predictive cellular bioinformatics
FILE REFERENCE: CytoP007C2
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Venkatakrishna, Shyamala
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: Endothelin B1 (ETB1) Receptor Polypeptide
TITLE OF INVENTION: Compositions, Methods, and Uses Thereof
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Psuedo-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 &
SOFTWARE: Word 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton Streeet
CITY: Emeryville
STATE: California
                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 21; Conserv
                                                                                                                                                             COUNTRY: US. ZIP: 946087
APPLICATION NUMBER:
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95.5%; Pred. No. 1.70
ative 0; Mismatches
US/08/117,361C
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Pred. No. 2e+02;
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RESULT 108
US-08-666-405-15
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                                    MEDIUM TYPE: FLUPRY CLORE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,405
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/EP94/04292
FILING DATE: 22-DEC-1994
PRIOR APPLICATION NUMBER: US 08/172,026
FILING DATE: 22-DEC-1994
PRIOR APPLICATION NUMBER: US 08/172,026
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: MUSERLIAN, CHARLES A
REFERENCE/DOCKET NUMBER: 102.164
TELEPHONE: (212) 661-8000
TELEPAX: (212) 661-8000
TELEPAX: (212) 661-8000
TELEPAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 15:
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APPLICANT: FACH, Patrick
APPLICANT: Jean-Pierre;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 923-2704
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: F TITLE OF INVENTION: F TITLE OF INVENTION: C TITLE OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: FLOPPY DISK
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CITY: NEW YORK
STATE: NEW YORK
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Local Similarity 95.5%;
ses 21; Conservation
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REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 09
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CLASSIFICATION:
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PRIMERS FOR THE
AMPLIFICATION OF GENES CODING FOR THE
ENTEROYDOXIN AND THE LECTHINASE OF CLOSTRID:
PERFRINGENS AND THEIR APPLICATION TO THE
DETECTION AND NUMERATION OF THESE BACTERIAE
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Pred. No. 2.4e+02;
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; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Clostridium perfringens
US-08-666-405-15
                                                                                                                                                                                                                                                                                                                                              RESULT 110
US-08-805-631A-6
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                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08805631A Patent No. 6096880
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LENGTH: 29
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APPLICANT: KOOL, ERIC T.
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity 88.0%;
Matches 22; Conservative
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EARLIER FILING DATE: 1995-02-23
EARLIER APPLICATION NUMBER: 08/047,860
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1997-02-26
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: UNIVER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          TITLE OF INVENTION:
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      STREET:
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                                                                                                                                                      SSEE: MUETING, RAASCH
T: 119 No. 6096880th I
Minneapolis
ARE: PatentIn Release #1.0, APPLICATION DATA:
                                                                                                        5540
                                                                                                                   Minnesota
Y: USA
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                                                                                                                                                                                                                                                                             UNIVERSITY OF ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%;
llarity 88.0%;
Conservative
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                                                                                                                                                                                                                                            DNA
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Pred. No. 3.3e+02;
0; Mismatches 3;
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Pred. No. 3.3e+02;
                                                                                                                                                                      E GEBHARDT, P.A. Fourth Street, Suite 201
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                Version #1.30
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RESULT 111
US-09-569-344-6
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Matches
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ATTORNEY AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.
TELECOMMUNICATION INFORMATION:
TELECHHONE: 612-305-1226
                                                                                       COMPUTER READABLE FOOM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-Msy-2000
CLASSIFICATION DATA:
APPLICATION UMBER: US 08/805,631
APPLICATION NUMBER: US 08/805,631
APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/803,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/393,439
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
UNINDERG UTGTTOTIA
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NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA
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22; Conserv
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larity 88.0%;
Conservative
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3.3e+02;
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                                                                                                                   US-08-146-504-16
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                                                   Matches
                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Heller, Michael J.; and Tu, Eugene TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICITIED OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND TITLE OF INVENTION: DIAGNOSTICS
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
                                            y PHALCH 0.3%; Score 20; DB 1; L
Local Similarity 100.0%; Pred. No. 1.6e+02;
hes 20; Conservative 0. Michigan
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
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4464 TITTTTTTTTTTTTTTTT 4483
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TYPE: nucleic acid
STRANDEDNESS: single
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611 West Sixth
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Pred. No. 3.3e+02;
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                                                                                 Length 20;
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US-08-379-593-5
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                                                                                                                                                 Sequence 16, Application US/08725976
Patent No. 5929208
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; ar
                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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OTHER INFORMATION:
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DESCRIPTION:
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NAME: Berridge, William P.
REGISTRATION UNMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: ///
CITY: Alexandria
CTATE: Virginia
                                                                                                               APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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                                                                               ADDRESSEE: Lyon & Lyon
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TITLE OF INVENTION: HAPTEN ASSAY DEVICE AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.ZIP: 22314
                              CITY: Los Angeles
STATE: California
                                                                 STREET:
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                 COUNTRY:
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                                                                 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cros, Philippe
Kurfurst, Robin
Battail, Nicole
                 USA
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other nucleic acid
/desc = "SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            consists of nucleosides with an alpha anomer and
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                          TT 4483
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US-08-997-080-83/c
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REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 222/;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPAX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 83, Appli
Patent No. 5968524
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: October 4, 1996
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 5929208ember 1, 1993
ANTORNEY/AGENT INFORMATION:
                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: WINDOWS (VERSION 3.0)
SOPTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/997,080 FILING DATE:
                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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100.0%; Pred. No.
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                                           11000.1007
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                                                                                                                              INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/997,362 FILING DATE:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970 FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Scott, Linda
APPLICANT: Prestridge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: Other
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                 TOPOLOGY: 11
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STREET: 20.
STREET: 20.
STREET: 20.
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OPERATING SYSTEM:
                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                               STRANDEDNESS:
                                                                                                                                                                TELEFAX: 206-269-0563
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STRANDEDNESS: single
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Visser, Elizabeth
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                                    linear
                                                   single
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Query Match

0.3%;

Score 20;

DB

1;

Length 20;

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; Sequence 83, Application US/08873970; Patent No. 6001361; GENERAL INFORMATION: APPLICANT: Tan, Paul APPLICANT: Hiyama, Jun APPLICANT: Visser, Elizabeth APPLICANT: Skinner, Margot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 117
US-08-965-780-1
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US-08-873-970-83/c
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/965,780
FILING DATE: 07-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 01931/97
FILING DATE: 18-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: KLDOVCIK, Ronald J.
REGISTRATION NUMBER: 25,401
REFERENCE/DOCKET NUMBER: FREI-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-887-90: TELEFAX: 202-887-9093 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Pitsch
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligoribonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: KUBOVCIK & KUBOVCIK
STREET: 900 17th Street, N.W., Suite 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weiss, Patrick A.
APPLICANT: Jenny, Luzi
TITLE OF INVENTION: RIBONUCLEOSIDE-DERIVATIVE AND METHOD FOR
TITLE OF INVENTION: PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             Local Similarity 0.0%; hes 0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 base pairs
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CITY: Washington
STATE: DC
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0.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                             20; Mismatches
                                                                                                                                                                                                                                                                                                                                    DB 1; Length 20;
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                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                               Patent No. 61500
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS;
CORRESPONDENCE ADDRESS;
The Correspondence Address of ann W. Speckman
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                        STATE:
                                                                                       CITY:
                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                        COUNTRY:
                                                                                                                   ADDRESSEE:
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20; Conservative
                                                                       NEW YORK
                                                                                                                                                                                                                                                                                           Application US/08765340
                                                                                                     345 PARK AVENUE
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                                                           USA
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                                                                                                                   MORGAN & FINNEGAN, L.L.P
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                                                                                                                                                                                                                                                                                                                                                                                                                          0.3%; Score 20; DB
100.0%; Pred. No. 1.0
ive 0; Mismatches
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PatentIn Release #1.0, Version

PC-DOS/MS-DOS

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US-09-095-855-83/c
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Best Local Similarity
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF CONTRESON OF ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 1: FILING DATE: 27-JUN-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 3:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DO SOFTWARE: PATENTIN Relu SOFTWARE: #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4464 TTTTTTTTTTTTTTTTTT 4483
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100.0%; Pred. No.
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1.6e+02;
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, ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo
US-09-407-675-1
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US-09-407-675-1/c
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Sequence 1, Application US/09250075
Patent No. 6207819
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Maier, Martin A
APPLICANT: Maier, Martin A
TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis
TITLE OF INVENTION: Mixed Backbone Oligomeric Compounds
                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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Best Local Similarity
Matches 20; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bruice, Thomas C.
APPLICANT: Arya, Dev P.
APPLICANT: Arya, Dev P.
TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIOUREA COMPOUNDS AND USES THEREOF
FILE REFERENCE: 30448.65US02
CURRENT APPLICATION NUMBER: US/09/407,675
CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 09/347,443
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091,481
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-17-01
PRIOR FILING DATE: 1998-17-01
PRIOR FILING DATE: 1998-17-02
PRIOR FILING DATE: 1998-17-01
                                                                                                                                                                                                                                                                                                                                            Query Match
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NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 20
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                                                                                                                                                                                                                                                                                                                       Local
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TOPOLOGY: lir
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Bruice, IL.
Dev P.
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0:
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US-09-173-936B-14
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                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.50 inch Diskette

COMPUTER: IBM-MS

OPERATING SYSTEM: Window 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/173,936B

FILING DATE: 16-Oct-1998

CLASSIFICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION DATA:

APPLICATION NUMBER: 60/063,757

PILING DATE: 17-OCT-1997

INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 20
                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Applicatio Patent No. 6238865
GENERAL INFORMATION:
APPLICANT: Zhen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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NAME/KEY: misc feature

LOCATION: (1)...(19)

OTHER INFORMATION: 2'-methoxyethoxy (MOE)

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Cohen, Pontani, Lieberman & Pavane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhen, Huang; Szostak, Jack W.
TITLE OF INVENTION: A Simple and Efficient Method to Label and Modify 3'-
Terminal
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 21
                                   4464 TITTTTTTTTTTTTTTT 4483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 551 Fifth Avenue
 TTTTTTTTTTTTTTTTTT 20
                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                          Conservative
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100.0%; Pred. No. 1.6e+02;
                                                                        0.3%; Score 20; DB 1; L
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                      14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Polymerase and a Synthetic Template with
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                                                                                                           Length 20;
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US-09-205-426-83/c

Sequence 83, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

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US-09-324-542-83/c
; Sequence 83, Application US/09324542
; Patent No. 6328978
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US-09-454-704A-13/c
RESULT 126
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                                                                                                                                                                                             ; OTHER INFORMATION: Made in a lab US-09-324-542-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09454704A Patent No. 6274321
GENERRAL INFORMATION:
APPLICANT: Blumberg, Bruce
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LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 83
LENGTH: 20
                                                                                                                         Matches
                                                                                                                                       Query Match
Best Local (
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Best Local Similarity
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CURRENT FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: High TITLE OF INVENTION: CDNAS FILE REPERENCE: P-UC 3662
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disord FILE REFERENCE: 11000.1007c1 CURRENT APPLICATION NUMBER: US/09/324,542 CURRENT FILING DATE: 1999-06-02 EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D. APPLICANT: Tan, Paul L.J. APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                       Local Similarity
                                                                         4464 TITITITITITITITITIT 4483
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High Throughput Functional Screening
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100.0%; Pred. No.
                                                                                                                                         100.0%;
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100.0%; Pred. No. 1.
1ve 0; Mismatches
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1.6e+02
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FILE REFERENCE: 11000.1002c4

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APPLICANT: Kurz, Markus
APPLICANT: Lohse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: $0036/031002
CURRENT PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
NUMBER OF EQ ID NOS: 26
SOFTWARE: FastSEQ for Wir-
SEQ ID NO 26
LENGTH: 20
TYPE: DW'
OPC':
                                                                                            RESULT 128
US-09-726-096A-1
; Sequence 1, Application US/09726096A
; Patent No. 6462184
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EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/97,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
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LENGTH: 20
TYPE: DNA
                                            GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Maier, Martin A.
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Best Local
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Best Local
        TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed TITLE OF INVENTION: Oligomeric Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
FILE REFERENCE: ISIS4528
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CURRENT FILING DATE: 1998-12-04
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nes 20; Conserv
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Pred. No.
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1.6e+02;
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hes 0;
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SEQ ID NO 55
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-09-603-830-55/c
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                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:random; OTHER INFORMATION: synthetic sequence
US-09-603-830-55
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                                                                 Matches
                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO TITLE OF INVENTION: AND USES THEREFOR FILE REFERENCE: 4149-1-1-1 CURRENT APPLICATION NUMBER: US/09/603,830 CURRENT FILING DATE: 2000-06-26 CURRENT FILING DATE: 2000-06-26 PRIOR APPLICATION NUMBER: 60/031,809 PRIOR PILING DATE: 196-07-29 PRIOR FILING DATE: 196-07-29 PRIOR PILING DATE: 1997-07-21 PRIOR FILING DATE: 1997-07-21 PRIOR FILING DATE: 1997-07-21
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/240,755
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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TYPE: DNA
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Oligonucleotide
NAME/KEY: misc feature
LOCATION: (1)...(20)
OTHER INFORMATION: 2'-methoxyethoxy (MOE)
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Elghanian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Letsinger, Robert L.
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                                                                 Conservative
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100.0%; Pred. No.
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RESULT 130 US-09-976-978A-55/c

GENERAL INFORMATION:

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Application US/09976978A

APPLICANT: Mirkin, Chad A.

Letsinger, Robert L. Mucic, Robert C.

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                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/016,520
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 10
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09344260A Patent No. 6576752 GENERAL INFORMATION:
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Query Match
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PRIOR APPLICATION NUMBER: 09/603,830
PRIOR FILING DATE: 2000-6-26
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                               APPLICANT: Salo, Harri
APPLICANT: Virta, Pasi
TITLE OF THE TON: Aminoxy Functionalized Oligomers
FILE REFERENCE: ISIS-3508
CURRENT APPLICATION NUMBER: US/09/344,260A
CURRENT FILING DATE: 1999-06-25
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PRIOR FILING DATE: 2000-04-26
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PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO TITLE OF INVENTION: AND USES THEREFOR FILE REFERENCE: 00-713-117
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Manoharan, Muthiah APPLICANT: Lonnberg, Harri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US97/12783
PRIOR FILING DATE: 1997-07-21
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                                                            OTHER INFORMATION: No.
                                                                           PEATURE: misc_feature
                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:random OTHER INFORMATION: synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Storhoff, James J.
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Pred. No.
Score 20;
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  BB
1;
Length 20;
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CURRENT APPLICATION NUMBER: US/09/961,949A
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 09/603,830
PRIOR FILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: PCT/US97/12783
PRIOR APPLICATION NUMBER: 60/031,809
PRIOR FILING DATE: 1997-07-21
PRIOR FILING DATE: 1996-07-29
PRIOR FILING DATE: 1996-07-29
PRIOR FILING DATE: 1996-07-29
                                                                                                                                                                                                                                                     Sequence 55, Application US/09966491A Patent No. 6610491 GENERAL INFORMATION:
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LENGTH: 20
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Best Local Similarity
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                                                   APPLICANT: Letsinger, Robert L.
APPLICANT: Mucic, Robert C.
APPLICANT: Storhoff, James J.
APPLICANT: Elghanian, Robert
APPLICANT: Taton, Thomas A.
APPLICANT: Taton, Thomas A.
TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
TITLE OF INVENTION: AND USES THEREFOR
TILE REFERENCE: 00-713-14
                                                                                                                                                                 APPLICANT: Mirkin, Chad A.
APPLICANT: Letsinger, Rob
APPLICANT: Mucic, Robert
APPLICANT: Storhoff, Jame
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PRIOR FILING DATE: 2000-04-26
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                 CURRENT APPLICATION NUMBER: US/09/966,491A CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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PRIOR APPLICATION NUMBER: 09/603,830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Description of Artificial Sequence:random OTHER INFORMATION: synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Mucic, Robert C.
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ive 0; Mismatches 0;
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/957,313A
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/603,830
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 07/US97/12783
PRIOR APPLICATION NUMBER: 60/031,809
PRIOR PILING DATE: 1997-07-29
PRIOR FILING DATE: 1996-07-29
PRIOR FILING DATE: 1996-07-29
PRIOR FILING DATE: 1996-07-29
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SOFTWARE: Microsoft Word 2000
SEQ ID NO 55
LENGTH: 20
Query Match 0.3%; Score 20; DB 1; Let Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/09957313A Patent No. 6645721
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LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.3%; Score 20; DB 1; Best Local Similarity 100.0%; Pred. No. 1.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taton, Thomas A.
TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLECTIDES ATTACHED THERETO
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 00-713-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: PCT/US97/12783
PRIOR FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/031,809
PRIOR FILING DATE: 1996-07-29
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/200,161 PRIOR FILING DATE: 2000-04-26
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PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Microsoft Word 2000
                                                                                                                   ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:random
OTHER INFORMATION: synthetic sequence
                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: SIGNIOIL, CAMBOD.

APPLICANT: Elghanian, Robert

APPLICANT: Taton, Thomas A.

TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: 00-713-15

CURRENT PAPLICATION NUMBER: US/09/966,312

CURRENT APPLICATION NUMBER: 09/603,830

PRIOR APPLICATION NUMBER: 09/344,667

PRIOR APPLICATION NUMBER: 09/344,667

PRIOR FILING DATE: 1990-06-26

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 09/240,755

PRIOR APPLICATION NUMBER: 09/240,755

PRIOR PILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/031,809

PRIOR APPLICATION NUMBER: 60/031,809

PRIOR FILING DATE: 1996-07-21

PRIOR APPLICATION NUMBER: 60/200,161

PRIOR APPLICATION NUMBER: 60/200,161

PRIOR FILING DATE: 1996-07-29

PRIOR FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Microsoft Word 2000

SEQ ID NO 55

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-312-55
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GENERAL INFORMATION:
APPLICANT: Mirkin, Chad A.
APPLICANT: Mirkin, Chad A.
APPLICANT: Letsinger, Robert C.
APPLICANT: Mucic, Robert C.
APPLICANT: Storhoff, James J.
APPLICANT: Storhoff, James J.
APPLICANT: Taton, Thomas A.
TITLE OF INVENTION: ANDOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 00-713-i11
CURRENT APPLICATION NUMBER: US/09/975,062A
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/603,830
PRIOR APPLICATION NUMBER: 09/603,830
PRIOR APPLICATION NUMBER: 09/603,830
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Best Local
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.3%; Score 20;
100.0%; Pred. No.
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FILING DATE: 1999-06-25

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TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 00-713-118
CURRENT APPLICATION NUMBER: US/09/976,971A
CURRENT APPLICATION NUMBER: US/09/976,971A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/63,830
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR APPLICATION NUMBER: 09/344,667
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR APPLICATION NUMBER: 05/200,755
PRIOR APPLICATION NUMBER: 05/200,761
PRIOR PILING DATE: 1997-07-21
PRIOR PILING DATE: 1997-07-21
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 1996-07-29
PRIOR PILING DATE: 2000-04-26
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                                                                                                                                   ; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:random
OTHER INFORMATION: synthetic sequence
US-09-976-971A-55
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US-09-976-971A-55/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 2000
SEQ ID NO 55
LENGTH: 20
                                           Matches
                                                                  Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                    SEQ ID NO 55
LENGTH: 20
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APPLICANT: Letsinger, F
APPLICANT: Mucic, Rober
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SOFTWARE, M:
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PRIOR FILING DATE: 2000-04-26
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                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US97/12783
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  4464 TTTTTTTTTTTTTTTTTTT 4483
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Taton, Thomas A.
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                                              Conservative
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                                                                0.3%; Score 20;
100.0%; Pred. No.
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                           0,
                                              Mismatches
                                                                                       DB 1;
                                                                  1.6e+02;
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                                           0,
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                                           Gaps
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                                                                                                                                                                        Sequence 2, Application US/08146504
Patent No. 5605662
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/930,087
APPLICATION NUMBER: US 07/930,087
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M0636/70071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 617-720-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                     APPLICANT: Heller, Michael J.; and Tu, Eugene TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND TITLE OF INVENTION: DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic RNA oligonucleotide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
ANTI-SENSE: 1
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                                       CORRESPONDENCE ADDRESS:
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ADDRESSEE:
STREET: 61
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E: Lyon & Lyon
611 West Sixth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      0.3%; Score 20;
00.0%; Pred. No.
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ZIP: 90017

COUNTRY:

California

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RESULT 140
US-08-455-896-13
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Best Local Similarity
Matches 20; Conserva
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MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,504
PILING DATE: No. 5605662ember 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
APPLICATION NUMBER: US/08/455,896
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 952726
                                                                                                                                ZIP: 63105-1817

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
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LENGTH: 21
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                         CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                     USA
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llarity 100.0%; F
Conservative 0;
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US-08-933-149-13
                                                                                          US-08-933-149-13
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                             Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: WATSON, MAPPLICANT: PLEMING, I
TITLE OF INVENTION: MATTITLE OF INVENTION: MATTITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Appli
Patent No. 5922836
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                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HENDERSON, MELODIE W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
                                                                                                                                                                                                           TELEFAX: (314) 727-609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314) 727-609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,149
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                MOLECULE TYPE:
                                                                                                     HYPOTHETICAL:
ANTI-SENSE: 1
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                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 63105-1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 77
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STRANDEDNESS: sing
                                                                                                                                                               STRANDEDNESS:
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 4464 TITTITTTTTTTTTTTTT 4483
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application
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7733 FORSYTH BOULEVARD, SUITE 1400
                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MARK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIMOTHY P. MAMMAGLOBIN,
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                                           Score 20; ; Pred. No.
                               0; Mismatches
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Pred. No.
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                                           1.8e+02;
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RESULT 143
US-09-082-343-13
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Patent No. 5929208
GENERAL INFORMATION:
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Patent No. 5968754
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
APPLICANT: FLEMING: DNA SEQUENCE AND ENCODED
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application APPLICATION DATA: described below:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 5929208ember 1, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS (VERSION
SOFTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Heller, Michael J.; and Tu, Eugene TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
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                                                                                                                                  NUMBER OF SEQUENCES:
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Local Similarity 100.0%;
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CITY: Los Angeles
STATE: California
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REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/72: FILING DATE: October 4, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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TELEFAX: 67-3510
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                                   STATE:
                                                       CITY: ST. LOUIS
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                                                                       ADDRESSEE: ROGERS, HOWELL & HAFERKAMP
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
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633 West Fifth Street
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A: described below:
08/146,504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5981185
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 1185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDN HYPOTHETICAL: NO ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,343
                                                                                                                           SOFTWARE: COREI WOLLL---
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMBER: US/08/863,639A
                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matson, Robert S. APPLICANT: Coassin, Peter J. APPLICANT: Rampal, Jang B. APPLICANT: Caskey, C. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,896
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                        STREET: 222
                                                                                                   APPLICATION NUMBER: US/08, FILING DATE: May 28, 1997 CLASSIFICATION: 435
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                                                                                                                                                                                     COMPUTER: IBM compatible OPERATING SYSTEM: Window
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ZIP: 91101
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NENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
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100.0%; Pred. No.
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